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OM protein - protein search, using sw model

Run on: April 15, 2003, 12:01:27 ; Search time 131 Seconds
(without alignments)
189.942 Million cell updates/sec

Title: US-10-017-372E-37

Perfect score: 1 MATSGRLPLPLMLLV.....GRKPVEQLSMIVRSCKS 407

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 0%

Listing first 45 summaries

Database :

Published Applications-AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2030.5	94.0	390	9	US-09-214-592-26
2	1929.5	89.4	390	9	US-09-214-592-29
3	1914.5	88.7	390	9	US-09-214-592-33
4	1909	88.3	391	9	US-09-214-592-17
5	1905.5	88.3	390	10	US-09-756-283A-23
6	1893.5	87.7	390	9	US-09-214-592-28
7	1893.5	85.0	390	9	US-09-214-592-20
8	1835.5	85.0	390	9	US-09-214-592-23
9	1572.5	72.8	315	9	US-09-214-592-25
10	1262.5	58.5	455	10	US-09-756-283A-20
11	1139	52.8	447	10	US-09-756-283A-22
12	1047	48.5	373	9	US-09-214-592-32
13	871.5	40.4	412	9	US-09-214-592-31
14	868.5	40.2	382	9	US-09-214-592-34
15	868	40.2	383	10	US-09-756-283A-27
16	834	38.6	409	9	US-09-214-592-27
17	827.5	38.3	410	9	US-09-214-592-22
18	826.5	38.3	412	9	US-09-214-592-24
19	824.5	38.2	412	9	US-09-214-592-19

20	824.5	38.2	412	12	US-10-028-158-21	Sequence 21, Appl
21	824	38.2	414	9	US-09-214-592-21	Sequence 21, Appl
22	820.5	38.0	412	10	US-09-756-283A-25	Sequence 25, Appl
23	809	37.5	414	9	US-09-214-592-18	Sequence 18, Appl
24	809	37.5	414	10	US-09-756-283A-24	Sequence 24, Appl
25	808	37.4	412	9	US-09-214-592-30	Sequence 30, Appl
26	792	36.7	304	10	US-09-756-283A-26	Sequence 26, Appl
27	753.5	34.9	139	12	US-10-002-278-8	Sequence 8, Appl1
28	638	29.6	112	9	US-09-813-398-13	Sequence 13, Appl1
29	638	29.6	114	10	US-09-813-459-22	Sequence 22, Appl
30	638	29.6	114	10	US-10-115-406-21	Sequence 21, Appl
31	638	29.6	114	12	US-09-813-271B-6	Sequence 47, Appl
32	638	29.6	115	9	US-09-859-211-47	Sequence 25, Appl
33	638	29.6	115	9	US-09-880-708-25	Sequence 25, Appl
34	542	25.1	116	12	US-10-115-406-24	Sequence 8, Appl1
35	535	24.8	112	10	US-09-813-271B-8	Sequence 13, Appl1
36	504	23.3	112	10	US-09-813-406-25	Sequence 25, Appl
37	504	23.3	114	12	US-10-115-406-25	Sequence 6, Appl1
38	500	23.2	112	9	US-09-813-271B-6	Sequence 15, Appl
39	500	23.2	113	10	US-09-813-398-15	Sequence 24, Appl
40	500	23.2	114	10	US-09-813-459-24	Sequence 23, Appl
41	500	23.2	114	12	US-10-115-406-23	Sequence 27, Appl
42	500	23.2	115	9	US-09-880-708-27	Sequence 49, Appl
43	493	22.8	115	9	US-09-859-211-49	Sequence 4, Appl1
44	482	22.3	112	10	US-09-813-271B-4	Sequence 14, Appl
45	482	22.3	113	9	US-09-813-398-14	

ALIGNMENTS

```
RESULT 1
US-09-214-592-26
Sequence 26, Application US/09214592A
Publication No. US20030027218A1
GENERAL INFORMATION:
APPLICANT: Yamasaki, CMCotoo
APPLICANT: Shibata, Ckenji
APPLICANT: Sato, Cyesutumi
TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
FILE REFERENCE: 11060
CURRENT APPLICATION NUMBER: US/09/214,592A
CURRENT FILING DATE: 1999-01-18
NUMBER OF SEQ ID NOS: 34
SOFTWARE:
SEQ ID NO 26
LENGTH: 390
TYPE: PRT
ORGANISM: porcine
US-09-214-592-26

Query Match          94.0%  Score 2030.5; DB 9; Length 390;
Best Local Similarity 94.8%  Pred. No. 9e+165;
Matches 386; Conservative 1; Mismatches 3; Indels 17; Gaps 1;
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1 MATSGRLPLPLMLLVLPGRPAAGISTCKTIDMELVKKRRIRAIKQILSKRLA 60

1 MPPSGRLPLPLMLLVLPGRPAAGISTCKTIDMELVKKRRIRAIKQILSKRLA 60

61 SPPSGDVPGRPELVNLVNSTRDVAGESEVPEPEPADYAKVTRILWESGNOI 120

61 SPPSGDVPGRPELVNLVNSTRDVAGESEVPEPEPADYAKVTRILWESGNOI 120

121 YKFKGTPSHLYMLFNTSELREAVPEPVLLSRALRLRLKLVQHEVLKYKISND 180

121 YKFKGTPSHLYMLFNTSELREAVPEPVLLSRALRLRLKLVQHEVLKYKISND 180

181 YSNRLAPSDSEPMISFDYTGVRQMLTRREALTEGRILSAHSSDSKDNTHVEINGFN 240

181 YSNRLAPSDSEPMISFDYTGVRQMLTRREALTEGRILSAHSSDSKDNTHVEINGFN 240

241 SGRGDLATIHGNRRPLLMATPLERAOHLHSSRRRAADLTNSYPYDVPDASTALDTN 300

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Db 241 SGRGDLATIHGMRPFLMATPLERAQHLSSRRH-----ALDTN 283
QY 301 YCFSTKNCVROLYIDFRKDLGKWIHEPKGYHANFCGPGYIWSLDTOYSKVALY 360
Db 284 YCFSTKNCVROLYIDFRKDLGKWIHEPKGYHANFCGPGYIWSLDTOYSKVALY 343
QY 361 NOHNPASAPCCVPOALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
Db 344 NOHNPASAPCCVPOALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390

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RESULT 2
US-09-214-592-29

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; Sequence 29, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, CMOtoo
; APPLICANT: Shibata, Ckenji
; APPLICANT: Sato, Ctasufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 29
; LENGTH: 390
; TYPE: PRT
; ORGANISM: ovine
US-09-214-592-29

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Query Match 89.4%; Score 1929.5; DB 9; Length 390;
Best Local Similarity 89.7%; Pred. No. 3.5e-156;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

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QY 1 MAPSGRLPLPLPLMLVLTPGRPAAGLSTCKTIMELVKRRRIETIRGOILSKRLA 60
Db 1 MPSSGRLPLPLPLMLMLTPGRPAAGLSTCKTIMELVKRRRIETIRGOILSKRLA 60
QY 61 SPSSQGDVPPGPLEAVLALYNSTRDRVAGESEVEPEPEADYYAKETRYLWVESGNOI 120
Db 61 SPSSQGDVPPGPLEAVLALYNSTRDRVAGESEVEPEPEADYYAKETRYLWVESGNOI 120
QY 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRARLRLRLKLYEQHVELYOKYSNDSWR 180
Db 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRARLRLRLKLYEQHVELYOKYSNDSWR 180
QY 181 YLSNRLAPSDSEWLSFDVTGVVROWLITRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Db 181 YLSNRLAPSDSEWLSFDVTGVVROWLITRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
QY 241 SGRGDLATIHGMRPFLMATPLERAQHLSSRRHRAALDTNSYPYDVPDYLADLTN 300
Db 241 SGRGDLATIHGMRPFLMATPLERAQHLSSRRHRAALDTNSYPYDVPDYLADLTN 300
QY 301 YCFSTKNCVROLYIDFRKDLGKWIHEPKGYHANFCGPGYIWSLDTOYSKVALY 360
Db 301 YCFSTKNCVROLYIDFRKDLGKWIHEPKGYHANFCGPGYIWSLDTOYSKVALY 360
QY 361 NOHNPASAPCCVPOALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
Db 361 NOHNPASAPCCVPOALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390

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RESULT 3
US-09-214-592-33

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; Sequence 33, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, CMOtoo
; APPLICANT: Shibata, Ckenji

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; APPLICANT: Sato, Ctasufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 33
; LENGTH: 390
; TYPE: PRT
; ORGANISM: simian
US-09-214-592-33

```

Query Match 88.7%; Score 1914.5; DB 9; Length 390;
Best Local Similarity 89.4%; Pred. No. 6.6e-155;
Matches 364; Conservative 10; Mismatches 16; Indels 17; Gaps 1;

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QY 1 MAPSGRLPLPLPLMLVLTPGRPAAGLSTCKTIMELVKRRRIETIRGOILSKRLA 60
Db 1 MPSSGRLPLPLPLMLMLTPGRPAAGLSTCKTIMELVKRRRIETIRGOILSKRLA 60
QY 61 SPSSQGDVPPGPLEAVLALYNSTRDRVAGESEVEPEPEADYYAKETRYLWVESGNOI 120
Db 61 SPSSQGDVPPGPLEAVLALYNSTRDRVAGESEVEPEPEADYYAKETRYLWVESGNOI 120
QY 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRARLRLRLKLYEQHVELYOKYSNDSWR 180
Db 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRARLRLRLKLYEQHVELYOKYSNDSWR 180
QY 181 YLSNRLAPSDSEWLSFDVTGVVROWLITRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Db 181 YLSNRLAPSDSEWLSFDVTGVVROWLITRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
QY 241 SGRGDLATIHGMRPFLMATPLERAQHLSSRRHRAALDTNSYPYDVPDYLADLTN 300
Db 241 SGRGDLATIHGMRPFLMATPLERAQHLSSRRHRAALDTNSYPYDVPDYLADLTN 300
QY 301 YCFSTKNCVROLYIDFRKDLGKWIHEPKGYHANFCGPGYIWSLDTOYSKVALY 360
Db 301 YCFSTKNCVROLYIDFRKDLGKWIHEPKGYHANFCGPGYIWSLDTOYSKVALY 360
QY 361 NOHNPASAPCCVPOALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
Db 361 NOHNPASAPCCVPOALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390

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RESULT 4
US-09-214-592-17

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; Sequence 17, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, CMOtoo
; APPLICANT: Shibata, Ckenji
; APPLICANT: Sato, Ctasufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 17
; LENGTH: 391
; TYPE: PRT
; ORGANISM: human
US-09-214-592-17

```

Query Match 88.4%; Score 1909; DB 9; Length 391;
Best Local Similarity 89.5%; Pred. No. 1.9e-154;
Matches 365; Conservative 10; Mismatches 15; Indels 18; Gaps 2;

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QY 1 MAPSGRLPLPLPLMLVLTPGRPAAGLSTCKTIMELVKRRRIETIRGOILSKRLA 60

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Db      1  |||||||
OY      61  SPPSGDVPPLPEALVALYNSTRDRVAGESVEPEPEADYAKETRYLVAVESGNOI 120
        |||||||
Db      61  SPPSGGEVPPPLPEALVALYNSTRDRVAGESAEPPEADYAKETRYLVAVETHEI 120
OY      121  YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRL-RLKLKVEQHVLYOKYSNDSM 179
        |||||||
Db      121  YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLRLKLKVEQHVLYOKYSNDSM 180
OY      180  RYLSNRLIAPSDSPWLSFDYTGVRQWLTREALEGFRLSAHSSSDSKONTLHVEINGF 239
        |||||||
Db      181  RYLSNRLIAPSDSPWLSFDYTGVRQWLTREALEGFRLSAHSSSDSKONTLQVDINGF 240
OY      240  NSGRGDLATIHGMNRPFLMATPLERAQHLHSSRRRALDNTSYPYDVAISALDNT 239
        |||||||
Db      241  TTGRGDLATIHGMNRPFLMATPLERAQHLHSSRRRALDNTSYPYDVAISALDNT 283
OY      300  NYCSTTEKNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTOYSKVAL 359
        |||||||
Db      284  NYCSTTEKNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTOYSKVAL 343
OY      360  YNOHNPASAPCCVPOALEPLIYVYVGRKPKVEQLSNMIVRSCKS 407
        |||||||
Db      344  YNOHNPASAPCCVPOALEPLIYVYVGRKPKVEQLSNMIVRSCKS 391

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RESULT 5
US-09-756-283A-23

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; Sequence 23, Application US/09756283A
; Patent No. US20020151478A1
;
GENERAL INFORMATION:
; APPLICANT: Chernajovsky, Yuri
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Adams, Gillian
; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFERENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 390
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-756-283A-23

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Query Match 88.3%; Score 1905.5; DB 10; Length 390;
Best Local Similarity 89.2%; Pred. No. 3,8e-154;
Matches 363; Conservative 10; Mismatches 17; Indels 17; Gaps 1;

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OY      1  MAPSGRLPLPLPLMLVLTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
        |||||||
Db      1  MPSSGRLPLPLPLMLVLTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
OY      61  SPPSGDVPPLPEALVALYNSTRDRVAGESVEPEPEADYAKETRYLVAVESGNOI 120
        |||||||
Db      61  SPPSGGEVPPPLPEALVALYNSTRDRVAGESAEPPEADYAKETRYLVAVETHEI 120
OY      121  YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLKLKVEQHVLYOKYSNDSM 180
        |||||||
Db      121  YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLKLKVEQHVLYOKYSNDSM 180
OY      181  YLSNRLIAPSDSPWLSFDYTGVRQWLTREALEGFRLSAHSSSDSKONTLHVEINGF 240
        |||||||
Db      181  YLSNRLIAPSDSPWLSFDYTGVRQWLTREALEGFRLSAHSSSDSKONTLQVDINGF 240
OY      241  SGRGDLATIHGMNRPFLMATPLERAQHLHSSRRRALDNTSYPYDVAISALDNT 300
        |||||||
Db      241  TGRGDLATIHGMNRPFLMATPLERAQHLHSSRRRALDNTSYPYDVAISALDNT 283
OY      301  YCFSTTEKNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTOYSKVAL 360

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Db      284  YCFSTTEKNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTOYSKVAL 343
OY      361  YNOHNPASAPCCVPOALEPLIYVYVGRKPKVEQLSNMIVRSCKS 407
        |||||||
Db      344  YNOHNPASAPCCVPOALEPLIYVYVGRKPKVEQLSNMIVRSCKS 390

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RESULT 6
US-09-214-592-28

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; Sequence 28, Application US/09214592A
; Publication No. US20030027218A1
;
GENERAL INFORMATION:
; APPLICANT: Yamasaki, Motoo
; APPLICANT: Shibata, Kenji
; APPLICANT: Sato, Cytasumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 28
; LENGTH: 390
; TYPE: prt
; ORGANISM: canine
US-09-214-592-28

```

Query Match 87.7%; Score 1893.5; DB 9; Length 390;
Best Local Similarity 88.7%; Pred. No. 4e-153;
Matches 361; Conservative 12; Mismatches 17; Indels 17; Gaps 1;

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OY      1  MAPSGRLPLPLPLMLVLTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
        |||||||
Db      1  MPSSGRLPLPLPLMLVLTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
OY      61  SPPSGDVPPLPEALVALYNSTRDRVAGESVEPEPEADYAKETRYLVAVESGNOI 120
        |||||||
Db      61  SPPSGGEVPPPLPEALVALYNSTRDRVAGESAEPPEADYAKETRYLVAVETHEI 120
OY      121  YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLKLKVEQHVLYOKYSNDSM 180
        |||||||
Db      121  YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLKLKVEQHVLYOKYSNDSM 180
OY      181  YLSNRLIAPSDSPWLSFDYTGVRQWLTREALEGFRLSAHSSSDSKONTLHVEINGF 240
        |||||||
Db      181  YLSNRLIAPSDSPWLSFDYTGVRQWLTREALEGFRLSAHSSSDSKONTLQVDINGF 240
OY      241  SGRGDLATIHGMNRPFLMATPLERAQHLHSSRRRALDNTSYPYDVAISALDNT 300
        |||||||
Db      241  SRRGDLATIHGMNRPFLMATPLERAQHLHSSRRRALDNTSYPYDVAISALDNT 283
OY      301  YCFSTTEKNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTOYSKVAL 360
        |||||||
Db      284  YCFSTTEKNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTOYSKVAL 343
OY      361  YNOHNPASAPCCVPOALEPLIYVYVGRKPKVEQLSNMIVRSCKS 407
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Db      344  YNOHNPASAPCCVPOALEPLIYVYVGRKPKVEQLSNMIVRSCKS 390

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RESULT 7
US-09-214-592-20

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; Sequence 20, Application US/09214592A
; Publication No. US20030027218A1
;
GENERAL INFORMATION:
; APPLICANT: Yamasaki, Motoo
; APPLICANT: Shibata, Kenji
; APPLICANT: Sato, Cytasumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
; FILE REFERENCE: 11060

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; CURRENT APPLICATION NUMBER: US/09/214,592A
 ; CURRENT FILING DATE: 1999-01-18
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE:
 ; SEQ ID NO 20
 ; LENGTH: 390
 ; TYPE: PR1
 ; ORGANISM: murine
 US-09-214-592-20

Query Match 85.0%; Score 1835.5; DB 9; Length 390;
 Best Local Similarity 85.0%; Pred. No. 3.4e-148;
 Matches 346; Conservative 15; Mismatches 29; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
 DB 1 MPSPGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
 QY 61 SPSPGQGVPPGPPLPEAVLALYNSTRDRVAGSADPEPEPADYYAKETRYLMDRNNAI 120
 DB 61 SPSPGQGVPPGPPLPEAVLALYNSTRDRVAGSADPEPEPADYYAKETRYLMDRNNAI 120
 QY 121 YDFKGTPHSLYMLFNTSELREAVPEVLLSRALRLRLKLTQEHVELYOKYSNDSWR 180
 DB 121 YDKTKDITSHIYMFNTSDIREAVPEPPLLSRAELRLQRLKSVQEHVELYOKYSNNSWR 180
 QY 181 YLSNRLAPSDPEWLSFDVTGVVROWLTRREALIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 DB 181 YLGNRLITPTDPEWLSFDVTGVVROWLTRREALIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 QY 241 YLGNRLITPTDPEWLSFDVTGVVROWLTRREALIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 DB 241 YLGNRLITPTDPEWLSFDVTGVVROWLTRREALIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 QY 241 YLGNRLITPTDPEWLSFDVTGVVROWLTRREALIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 DB 241 YLGNRLITPTDPEWLSFDVTGVVROWLTRREALIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 QY 301 YCFSTTEKNCVQOLYIDFKKDLGKWIHEPKGYHANFCIGPCPYIWSLDTQYSKVLA 360
 DB 301 YCFSTTEKNCVQOLYIDFKKDLGKWIHEPKGYHANFCIGPCPYIWSLDTQYSKVLA 360
 QY 284 YCFSTTEKNCVQOLYIDFKKDLGKWIHEPKGYHANFCIGPCPYIWSLDTQYSKVLA 343
 DB 284 YCFSTTEKNCVQOLYIDFKKDLGKWIHEPKGYHANFCIGPCPYIWSLDTQYSKVLA 343
 QY 361 NQHPGASAPCCVQALPEPLPIVYVGRKPKVEQLSNMIVRSCKS 407
 DB 344 NQHPGASAPCCVQALPEPLPIVYVGRKPKVEQLSNMIVRSCKS 390

RESULT 8

US-09-214-592-23
 ; Sequence 23, Application US/09214592A
 ; Publication No. US20030027218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yamasaki, Cmotoo
 ; APPLICANT: Shibata, Ckenji
 ; APPLICANT: Sato, Cyasufumi
 ; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
 ; FILE REFERENCE: 11060
 ; CURRENT APPLICATION NUMBER: US/09/214,592A
 ; CURRENT FILING DATE: 1999-01-18
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE:
 ; SEQ ID NO 23
 ; LENGTH: 390
 ; TYPE: PR1
 ; ORGANISM: rat
 US-09-214-592-23

Query Match 85.0%; Score 1835.5; DB 9; Length 390;
 Best Local Similarity 85.0%; Pred. No. 3.4e-148;
 Matches 346; Conservative 14; Mismatches 30; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
 DB 1 MPSPGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
 QY 61 SPSPGQGVPPGPPLPEAVLALYNSTRDRVAGSADPEPEPADYYAKETRYLMDRNNAI 120

DB 61 SPSPGQGVPPGPPLPEAVLALYNSTRDRVAGSADPEPEPADYYAKETRYLMDRNNAI 120
 QY 121 YDFKGTPHSLYMLFNTSELREAVPEVLLSRALRLRLKLTQEHVELYOKYSNDSWR 180
 DB 121 YDKTKDITSHIYMFNTSDIREAVPEPPLLSRAELRLQRLKSVQEHVELYOKYSNNSWR 180
 QY 181 YLSNRLAPSDPEWLSFDVTGVVROWLTRREALIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 DB 181 YLGNRLITPTDPEWLSFDVTGVVROWLTRREALIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 QY 241 YLGNRLITPTDPEWLSFDVTGVVROWLTRREALIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 DB 241 YLGNRLITPTDPEWLSFDVTGVVROWLTRREALIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 QY 241 YLGNRLITPTDPEWLSFDVTGVVROWLTRREALIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 DB 241 YLGNRLITPTDPEWLSFDVTGVVROWLTRREALIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 QY 301 YCFSTTEKNCVQOLYIDFKKDLGKWIHEPKGYHANFCIGPCPYIWSLDTQYSKVLA 360
 DB 284 YCFSTTEKNCVQOLYIDFKKDLGKWIHEPKGYHANFCIGPCPYIWSLDTQYSKVLA 343
 QY 361 NQHPGASAPCCVQALPEPLPIVYVGRKPKVEQLSNMIVRSCKS 407
 DB 344 NQHPGASAPCCVQALPEPLPIVYVGRKPKVEQLSNMIVRSCKS 390

RESULT 9

US-09-214-592-25
 ; Sequence 25, Application US/09214592A
 ; Publication No. US20030027218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yamasaki, Cmotoo
 ; APPLICANT: Shibata, Ckenji
 ; APPLICANT: Sato, Cyasufumi
 ; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
 ; FILE REFERENCE: 11060
 ; CURRENT APPLICATION NUMBER: US/09/214,592A
 ; CURRENT FILING DATE: 1999-01-18
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE:
 ; SEQ ID NO 25
 ; LENGTH: 315
 ; TYPE: PR1
 ; ORGANISM: bovine
 US-09-214-592-25

Query Match 72.8%; Score 1572.5; DB 9; Length 315;
 Best Local Similarity 88.9%; Pred. No. 6e-126;
 Matches 295; Conservative 9; Mismatches 11; Indels 17; Gaps 1;

QY 76 AVLALYNSTRDRVAGSADPEPEPADYYAKETRYLMDRNNAI 135
 DB 1 ALALYNSTRDRVAGSADPEPEPADYYAKETRYLMDRNNAI 60
 QY 136 NQHPGASAPCCVQALPEPLPIVYVGRKPKVEQLSNMIVRSCKS 195
 DB 61 NQHPGASAPCCVQALPEPLPIVYVGRKPKVEQLSNMIVRSCKS 120
 QY 196 LSFDTGVVROWLTRREALIEGFRLSAHSSSDSKDNTLHVEINGFN 255
 DB 121 LSFDTGVVROWLTRREALIEGFRLSAHSSSDSKDNTLHVEINGFN 180
 QY 256 PFLLMATPPLERAQHLHSSRRALDNTNSPYVDPYASIALDNTNCFSTTEKNCVROL 315
 DB 161 PFLLMATPPLERAQHLHSSRRALDNTNSPYVDPYASIALDNTNCFSTTEKNCVROL 223
 QY 316 YDFKGTPHSLYMLFNTSELREAVPEVLLSRALRLRLKLTQEHVELYOKYSNDSWR 375
 DB 224 YDFKGTPHSLYMLFNTSELREAVPEVLLSRALRLRLKLTQEHVELYOKYSNDSWR 283
 QY 376 QALEPLPIVYVGRKPKVEQLSNMIVRSCKS 407
 DB 284 QALEPLPIVYVGRKPKVEQLSNMIVRSCKS 315


```
RESULT 10
US-09-756-283A-20
; Sequence 20, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
; APPLICANT: Chernajovsky, Yuti
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Adams, Gillian
; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFERENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LAP-mIFN construct
US-09-756-283A-20

Query Match          52.8%; Score 1139; DB 10; Length 455;
Best Local Similarity 90.5%; Pred. No. 2,3e-99;
Matches 248; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

1  MAPSGRLRLPLLLPLMLLVLTTPGRPAAGLSTCKTIDMELVKKRIEAIKGLSKRLA 60
1  MPPSGRLRLPLLLPLMLLVLTTPGRPAAGLSTCKTIDMELVKKRIEAIKGLSKRLA 60
QY 61  SPPSGGVDPGRLPAVALYNSTRDVRVAGESVEPEPEADYAKEVTRVLAVESGNOI 120
QY 61  SPPSGGVDPGRLPAVALYNSTRDVRVAGESVEPEPEADYAKEVTRVLAVETINEI 120
DB 61  SPPSGGVDPGRLPAVALYNSTRDVRVAGESVEPEPEADYAKEVTRVLAVETINEI 120
QY 121 YDKEFGTSHSLYMLFNTSELREAVPEVLLSRAELRL-RLKLVEQHVLYOKYSNDSW 179
QY 121 YDKEFGTSHSLYMLFNTSELREAVPEVLLSRAELRL-RLKLVEQHVLYOKYSNDSW 179
DB 121 YDKEFGTSHSLYMLFNTSELREAVPEVLLSRAELRLRLKLVEQHVLYOKYSNDSW 180
QY 180 RLTSNRLAPSSPELSDVYGVYKQWLTTRRAIEGFRLSAHSKNTLHVEINGF 239
QY 181 RLTSNRLAPSSPELSDVYGVYKQWLTTRRAIEGFRLSAHSKNTLHVEINGF 240
DB 181 RLTSNRLAPSSPELSDVYGVYKQWLTTRRAIEGFRLSAHSKNTLHVEINGF 240
QY 240 NSGRGDLATIGMNRPFLLMATPLERAQHLS 273
QY 241 TIGRGGDLATIGMNRPFLLMATPLERAQHLS 274
DB 241 TIGRGGDLATIGMNRPFLLMATPLERAQHLS 274

RESULT 11
US-09-756-283A-22
; Sequence 22, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
; APPLICANT: Chernajovsky, Yuti
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Adams, Gillian
; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFERENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mIFN -LAP construct
US-09-756-283A-22

Query Match          52.8%; Score 1139; DB 10; Length 447;
Best Local Similarity 87.0%; Pred. No. 7,1e-89;
Matches 228; Conservative 10; Mismatches 18; Indels 6; Gaps 3;
```

```
QY 14 PL-LNLLVLTTPGRPAAGLSTCKTIDMELVKKRIEAIKGLSKRLASPPSGDVPGP 72
QY 190 PLGLW---AGGSAALSTCKTIDMELVKKRIEAIKGLSKRLASPPSGDVPGP 245
DB 190 PLGLW---AGGSAALSTCKTIDMELVKKRIEAIKGLSKRLASPPSGDVPGP 245
QY 73 LPEAVLALYNSTRDVRVAGESVEPEPEADYAKEVTRVLAVESGNOIYDKFKGPHSLY 132
QY 246 LPEAVLALYNSTRDVRVAGESVEPEPEADYAKEVTRVLAVETINEIYDKFKGPHSLY 305
DB 246 LPEAVLALYNSTRDVRVAGESVEPEPEADYAKEVTRVLAVETINEIYDKFKGPHSLY 305
QY 133 MLENVSELREAVPEVLLSRAELRL-RLKLVEQHVLYOKYSNDSMRYSNRLAPSD 191
DB 306 MLENVSELREAVPEVLLSRAELRLRLKLVEQHVLYOKYSNDSMRYSNRLAPSD 365
QY 192 SPEWLSFDVYGVYKQWLTTRRAIEGFRLSAHSKNTLHVEINGFNSGRGDLATIH 251
DB 366 SPEWLSFDVYGVYKQWLTTRRAIEGFRLSAHSKNTLHVEINGFNSGRGDLATIH 425
QY 252 GMRNPFLLMATPLERAQHLS 273
DB 426 GMRNPFLLMATPLERAQHLS 447

RESULT 12
US-09-214-592-32
; Sequence 32, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, Motoo
; APPLICANT: Shibata, Kenji
; APPLICANT: Sato, Chisatsumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 32
; LENGTH: 373
; TYPE: PRT
; ORGANISM: chicken
US-09-214-592-32

Query Match          48.5%; Score 1047; DB 9; Length 373;
Best Local Similarity 52.9%; Pred. No. 3,7e-81;
Matches 207; Conservative 52; Mismatches 100; Indels 32; Gaps 8;

QY 30 LSTCKTIDMELVKKRIEAIKGLSKRLASPPSGDVPGPRLPAVALYNSTRDVRV 89
DB 2 LSTCKTIDMELVKKRIEAIKGLSKRLASPPSGDVPGPRLPAVALYNSTRDVRV 61
QY 90 GRS-VEPEPEADYAKEVTRVLAVESGNOIYDKFKGPHSLYMLFNTSELREAVPEV 148
DB 62 GRARLRPPDPGDEYAKELRLRIPMETWIDGAMEHQPOSHSIFEFVNSRARRG-GRPT 120
QY 149 LLSRAELRLRLKLK-----VEQHVLYOKYSNDSMRYSNRLAPSDSEWLSFDVTG 203
DB 121 LLSRAELRLRLKAAADSAGTIDRLLYOGYGNASMYVLHGKRVYRATADEWLSFDVTG 180
QY 204 VQWOLTRRAIEGFRLSAHSKNTLHVEINGFNSGRGDLATIGMNR--PFL 258
DB 181 VQWOLTRRAIEGFRLSAHSKNTLHVEINGFNSGRGDLATIGMNR--PFL 239
QY 259 LMATPLERAQHLSRHRRALDPTNSYPYDVYASLADPTNCF--SSTFKNCVAVLY 316
DB 240 LMATPLERAQHLSRHRRALDPTNSYPYDVYASLADPTNCF--SSTFKNCVAVLY 282
QY 317 IDPKRLGKWKHEPKGYHANPCLGPOYIWSLDTQSKYALAYNQNPPASAPCCVPQ 376
DB 283 IDPKRLGKWKHEPKGYHANPCLGPOYIWSLDTQSKYALAYNQNPPASAPCCVPQ 342
QY 377 ALEPLPIVYVGRKPKVEQLSNMIVSCKS 407
DB 377 ALEPLPIVYVGRKPKVEQLSNMIVSCKS 407
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QY 123 KFKGTPHSLYMLFNTSPLREAVPERVLLSRAELRLRLK--KVEQHVELYOKYSNDSW- 179
Db 117 -----HEFKFKENASVREYVGNLSLHHAELMYKKOTDKNMDOHMLFWKYOENGT 170
QY 180 --RYLSNRLAPSDSPWLSFDVYGVVQWLTRREAIEGFRLSAH---SSDSKDNTLHV 234
Db 171 HSRYLESKYITPTVDDEMSPDYTKTVNEWMLKRAENEGFGLQPACKCPTPQAKD---I 226
QY 235 EINGFNSGRRGDLATIGHM--NRPFLLMATPLERAQHLHSSRRRALDTNSYPYDVPDY 292
Db 227 DIEGF-PALRGDLASLSKENTKPYLMTITSHPAERIDVTSSRRK----- 271
QY 293 ASIALDTNYCPSSTKNCQVQLYIDFRKDLGKWIHEPKGYHANFCLGPPYIWSLDTQ 352
Db 272 ---GVGOEYCTGNNGPCVYKPLIYINFRKDLGKWIHEPKGYEANYCLGNCPIYIMSDTQ 328
QY 353 YSKYLALYNQHNPGASAPCCVPOALEPLIYVYVGRKPKVEQLSNMIVRSCKS 407
Db 329 YSKVLSLYNNQNPASISPCCVPLLEPLIYVYVGRKPKVEQLSNMIVRSCKS 383
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Search completed: April 15, 2003, 12:04:30
Job time : 134 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:58:28 ; Search time 79 Seconds
(without alignments)
1061.534 Million cell updates/sec

Title: US-10-017-372E-37
Perfect score: 2159
Sequence: 1 MAPSGRLRLPLPLMLLV.....GRRKVEQLSNMIVRSCKS 407

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1815.5	84.1	390	6 Q9TUM8	Q9TUM8 equus caball
2	1736.5	80.4	368	11 Q8R4D9	Q8R4D9 sigmodon hi
3	827.5	38.3	412	11 Q91U07	Q91U07 mus musculu
4	825	38.2	382	13 Q9PWA9	Q9PWA9 morone chry
5	821	38.0	414	11 Q91VP5	Q91VP5 mus musculu
6	806	37.3	382	13 Q93449	Q93449 oncorhynch
7	780	36.1	376	13 Q9PT02	Q9PT02 cyprinus ca
8	760	35.2	399	11 Q9PBB7	Q9PBB7 mesocricetu
9	719.5	33.3	362	11 Q9PBB7	Q9PBB7 mus musculu
10	691.5	32.0	130	11 Q08714	Q08714 mesocricetu
11	674.5	31.2	124	6 Q95N80	Q95N80 canis fami1
12	673.5	31.2	361	13 Q98854	Q98854 cyprinus ca
13	638	29.6	112	6 Q02730	Q02730 oryctolagus
14	600	27.8	255	11 Q921T1	Q921T1 mus musculu
15	584.5	27.1	127	6 Q9TV08	Q9TV08 canis fami1
16	561.5	26.0	200	13 Q90YF1	Q90YF1 pleuronecte

17	554	25.7	101	11 Q9R184	Q9R184 meriones un
18	456	21.1	179	13 Q90YF2	Q90YF2 pleuronecte
19	413	19.1	88	13 Q90YF5	Q90YF5 pleuronecte
20	402	18.6	88	13 Q90YF7	Q90YF7 oncorhynch
21	397	18.4	88	13 Q90ZE7	Q90ZE7 acipenser b
22	393	18.2	87	13 Q42306	Q42306 carassius a
23	383	17.7	91	6 Q9MYZ1	Q9MYZ1 capra hircu
24	373	17.3	86	6 Q28241	Q28241 cervus elap
25	371.5	17.2	309	4 Q8WV88	Q8WV88 homo sapien
26	358	16.6	81	6 Q9NIS3	Q9NIS3 capreolus c
27	336.5	15.6	375	13 Q8UWD8	Q8UWD8 columba liv
28	321.5	14.9	375	13 Q8UWD7	Q8UWD7 coturnix ch
29	321.5	14.9	389	13 Q90YV0	Q90YV0 ictalurus p
30	317	14.7	77	13 Q90YF8	Q90YF8 oncorhynch
31	316.5	14.7	375	13 Q98SP0	Q98SP0 gallus gall
32	313.5	14.5	375	6 Q9GMY7	Q9GMY7 equus cabal
33	313.5	14.5	375	13 Q8UWE0	Q8UWE0 anas platyr
34	311.5	14.4	375	13 Q8UWD9	Q8UWD9 anser anser
35	306.5	14.2	56	6 Q95J86	Q95J86 macaca fasc
36	302	14.0	50	6 Q28240	Q28240 cervus elap
37	301	13.9	62	13 Q90ZJ7	Q90ZJ7 anguilla an
38	300	13.9	62	13 Q90YF4	Q90YF4 pleuronecte
39	296.5	13.7	375	6 Q8WNS6	Q8WNS6 bos taurus
40	295	13.7	376	13 Q98TB4	Q98TB4 oreochromis
41	294	13.6	376	13 Q90W06	Q90W06 umbrina cir
42	294	13.6	385	13 Q90W05	Q90W05 sparus aura
43	289.5	13.4	373	13 Q90ZD1	Q90ZD1 oncorhynch
44	287.5	13.3	377	13 Q98TB3	Q98TB3 morone chry
45	287	13.3	62	13 Q9DEP5	Q9DEP5 scophthalmu

ALIGNMENTS

RESULT 1

Q9TUM8 ID Q9TUM8 PRELIMINARY; PRT; 390 AA.

AC Q9TUM8; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Transforming growth factor beta 1.
GN TGFBI.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Nixon A.J., Brower-Toiland B.T., Sandell L.J.;
RT "Molecular cloning of equine transforming growth factor beta 1 reveals
RT a divergent nucleotide structure that encodes a novel bioactive
RT peptide among mammalian species.";
CC Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF175709; AAD49431.1; -.
DR HSSP; P01137; 1KLA.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb.N.
DR InterPro; IPR003911; TGF-TGFb.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR01423; TGFbBETA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Glycoprotein.

SEQUENCE 390 AA; 43860 MW; 220FE40DFCCA6016 CRC64;

Query Match 84.1%; Score 1815.5; DB 6; Length 390;
Best Local Similarity 85.5%; Pred. No. 3.1e-149;
Matches 348; Conservative 12; Mismatches 30; Indels 17; Gaps 1;


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OY 403 SCACS 407
DB 408 SCACS 412

RESULT 4
O9PMA9 PRELIMINARY; PRT: 382 AA.
AC O9PMA9;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Transforming growth factor beta precursor.
GN TGF-BETA.
OS Morone chrysops x Morone saxatilis (white bass x striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Moronidae; Morone.
OX NCBI_TaxID=45352;
RN [1]
RC SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=KIDNEY;
RX MEDLINE=20394636; PubMed=10938723;
RA Harms C.A., Kennedy-Stoskopf S., Horne W.A., Fuller F.J.,
RA Tompkins W.A.F.;
RT "Cloning and sequencing hybrid striped bass (Morone saxatilis x M.
RT chrysops) transforming growth factor-beta (TGF-beta), and development
RT of a reverse transcription quantitative competitive polymerase chain
RT reaction (RT-qPCR) assay to measure TGF-beta mRNA of teleost fish.";
RL Fish Shellfish Immunol. 10:61-85(2000).
CC -1- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGHER LEVELS FOUND IN MONONUCLEAR CELLS FROM
CC PERIPHERAL BLOOD THAN IN SPLEEN OR ANTERIOR KIDNEY.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL AF140363; AAD46997.1; -.
CC HSPB, P01137; IKA4.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1
FT PROPEP 270
FT CHAIN 271 382 TRANSFORMING GROWTH FACTOR BETA.
FT DISULFID 278 286 BY SIMILARITY.
FT DISULFID 285 348 BY SIMILARITY.
FT DISULFID 314 379 BY SIMILARITY.
FT DISULFID 318 381 BY SIMILARITY.
FT DISULFID 347 347 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 237 CELL ATTACHMENT SITE (POTENTIAL).
SQ SEQUENCE 382 AA; 43846 MW; 3124D8C34EA74D72 CRC64;

Query Match 38.2%; Score 825; DB 13; Length 382;
Best Local Similarity 45.3%; Pred. No. 2.8e-63;
Matches 186; Conservative 65; Mismatches 108; Indels 52; Gaps 15;
OY 15 LMLLVLTTPGRPAAGSTCKTIDMELVYKRRIRAIKQIISKLRL--ASPSOGDVP 71
DB 6 LMLVVYTVGN-VSGMSTCKTLDEWYKRRIRAIKQIISKLRLPKPEPDQADEBEI 64
OY 72 PLPEAVLALVNSRDRAVAGESVEPE-----PEPADYAKVTRVLMVESGNOIYDKRKG 126

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DB 65 PTP--LLSLYNSTKEMLKFOOTEVQTDISTEOEEEFYFAKVLAKENMTKRN----- 114
OY 127 TPRSLYKLENTSELREAVPEPVLLSRRLRLRLKLV--EQHVELYOKYNSDWRYSLN 184
DB 115 TDYTKKFEFNISELRESVGVDRLTSLAEIRMLIKTTIYDEQRELYSGL-GDSFRIYAS 173
OY 185 RLAPSDSPEMLSFDVYGVYROWLITREALEGF--RLSAHSSDSKDWTL-HVEINGENS 241
DB 174 RFTTNKKKKDKMLSFQVTKLQDWLKGTDDEGQFLRLCECNKVSAGETIFKFGISGIDP 233
OY 242 GRRODLATIGHMNR--PPLIMATPLERAQHLHS---SRHRALDTNSYPDVPYASLA 296
DB 234 G-RGDTGPMOLLTQOPPYILTMSP---QNISSPSYTSRKRKSTETK----- 275
OY 297 LDINVCSSSTEKNCCVQLYTDFRKDGKMWIHEKGYHANCPLGPCPYIMSLDTPYSKV 356
DB 276 --DVCAQGE--TCVNSLSYIDFRKDLGKMIHKRTGYINANTCMSCSYIIMNAEKYSOI 331
OY 357 LALYNOHNPGASAPCCVPALEPLPIVYVYGRKPRVQLSNMIVRSCKS 407
DB 332 LALKHHNPGASAPCCVPALEPLPIVYVYGRKPRVQLSNMIVRSCKS 382

RESULT 5
O91VP5 PRELIMINARY; PRT: 414 AA.
AC O91VP5;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Similar to transforming growth factor, beta 2.
GN TGFb2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL BC011170; AAH1170.1; -.
DR MGD; MG1:98726; Tgfb2.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR PROSITE: PS00250; TGF-BETA_1; UNKNOWN_1.
KW Glycoprotein.
SQ SEQUENCE 414 AA; 47588 MW; DB37A7C38881E286 CRC64;

Query Match 38.0%; Score 821; DB 11; Length 414;
Best Local Similarity 43.3%; Pred. No. 7.1e-63;
Matches 188; Conservative 62; Mismatches 122; Indels 62; Gaps 15;
OY 12 LPLMLLVLTTPGRPAAGSTCKTIDMELVYKRRIRAIKQIISKLRLASPSOGDVP-P 70
DB 5 VLSTFLHLHLV--VALSTGCTSLMDQFMKRIRAIKQIISKLRLSPPE--DYPEP 60
OY 71 GPLPEAVLALVNSRDRAVAGESVEPEPE--PEADYAKVETRYLM---VESGNOIYD 122
DB 61 DEVPEVISIYNSTRLDLEKASRRAAACERSSDELYAKVEYKIDMPSHLSENAIPP 120
OY 123 KFKGPHSLYLMFNTSELREAVPEPVLLSRRLRLRLKLV--EQHVELYQ-----K 173
DB 121 TRY-RPYKRIYRFDVSTMEKNSN---LYKAEFRVRLQPKRAVVAQRIELVQILSKSD 176
OY 174 YSNDSWRYLSNRLAPSDSPEMLSFDVYGVYROWLITREALEIGEFRLSAHSS----- 225
DB 177 LNSPTORYIDSKVYKTRAEGLMSLFDVTDAVOEMLHKKDRNLGKISLHCPCTFVPSNN 236

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Query Match	Best Local Similarity	Matches 182	Conservative 57	Mismatches 106	Indels 48	Gaps
37.3% Score 806; DB 13; Length 382;	46.3%; Pred. No. 1,3e-61;					
Db	30	182	57	106	48	86
QY	30	182	57	106	48	86
Db	23	182	57	106	48	80
QY	87	182	57	106	48	14
Db	81	182	57	106	48	12
QY	141	182	57	106	48	196
Db	130	182	57	106	48	186
QY	197	182	57	106	48	25
Db	189	182	57	106	48	247
QY	235	182	57	106	48	314
Db	248	182	57	106	48	283
QY	315	182	57	106	48	374
Db	290	182	57	106	48	349
QY	375	182	57	106	48	407
Db	350	182	57	106	48	382

[illegible]

CC -1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -1- SUBUNIT: HOMODIMER. DISULFIDE-BINDING.

CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECT
CC
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC

CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY
DR EMBL: X60296; CAA42838.1; -.
DR EMBL: AF046214; AAC40099.1; -.
DR HSSP: P01137. 1K1A

DR Pfam: PF00019; TGF-beta: 1
DR InterPro: IPR001839; TGFb.

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DR    FI100III; PD00035/; TGFb; 1.
DR    SMART; SM00204; TGFb; 1.
```

KW Growth factor; Mitogen; Glycoprotein.

FT	PROPEP	<1	18
EM	QUATN	10	100

FT	25	34	BY SIMILARITY,
DISULFID			
DISULFID	33	96	BY SIMILARITY,
FT			

FT	66	129	BY SIMILARITY.
DISULFID	95		INTERCHAIN (BY SIMILARITY)

71	CONFIDCI	93	G -> S (IN REF. 2).
SQ	SEQUENCE	130 AA;	14997 MW; 8B41DD6CF39CCA77 CRC64:

Query Match	32.08;	Score 691.5;	DB 11;	Length 130;
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Matches 127; Conservative 0; Mismatches 3; Indels 17;

261 MATPLERAQHLLSSRRRALDNTSYPIYDVPDYASLALDNTNYCFSSTEKNCVROLYID

DB 1 MA1PLERQHLTQSSRHR-----ALDTNYCFSTKNCVCVRLYID

221 IADJOWMWHTEFNGI HANE CUSGCFI IWSLDNY SKVLALYNQHNP CASAPCCVPOAL

[illegible]

104 TRIVVVCEKVEOI SMUTDZVZG 120

RESUL TI
Q95N80

AC Q95N80; ENI; 124 AA.

DT	01-DEC-2001 (Tremblé, 19, Last sequence update)
DT	01-JUN-2003 (Tremblé, 24, Last sequence update)

Transforming growth factor beta 1 (Fragment).

0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
0C Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis

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va mcbl_id=5013;
RN [1]
```

RA Fonfara S., Groene A., Baumgaertner W.;

RT cells, ";

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL: AF349538: AAK54072.1. -
DR

DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF-beta: 1.

DR PROSITE: PS00250; TGF_BETA_1; UNKNOWN_1.

FT	NON_TER	1	1
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SEQ SEQUENCE 124 AA; 14329 MW; 21D185218E5556DB CRC64;

1

Query Match 31.2%; Score 674.5; DB 6; Length 124;
 Best Local Similarity 87.2%; Pred. No. 6.6e-51;
 Matches 133; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

QY 264 PLERAQHLSRRRALDNTNSPYDVPDYASLALDNTNCFSSSTENKCCVROLXIDFRDL 323
 DB 1 PLERAQHLSRRQR-----ADNTNCFSSSTENKCCVROLXIDFRDL 43
 QY 324 GKWVHEPKGYHANFCLGCPGYIWSLDTQYSKVALYNQHNPGASAPCCVQALEPLPI 383
 DB 44 GKWVHEPKGYHANFCLGCPGYIWSLDTQYSKVALYNQHNPGASAPCCVQALEPLPI 103

QY 384 VYVGRKPKVEQLSNMIVRSC 404
 DB 104 VYVGRKPKVEQLSNMIVRSC 124

RESULT 12
 098854 PRELIMINARY; PRT; 361 AA.
 AC 098854;
 DT 01-FEB-1997 (Tremblrel. 02, Created)
 DT 01-FEB-1997 (Tremblrel. 02, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Transforming growth factor beta 2 (TGF-beta 2) (Fragment).
 OS *Cyprinus carpio* (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 NC NCBL_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RX MEDLINE=97354301; PubMed=9210595;
 RA Sumathi K., Desai K.V., Kondiah P.;
 RT "Isolation of transforming growth factor-beta2 cDNA from a fish,
 RT *Cyprinus carpio* by RT-PCR."
 RL Gene 191:103-107(1997).
 CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
 CC DEPENDENT T-CELL GROWTH.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL: U66874; AAB62983.1; -
 DR HSSP: P08112; 2TGI.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb.N.
 DR Pfam: PF00688; TGF-beta; 1.
 DR Pfam: PF00688; TGFb.propeptide; 1.
 DR ProDom: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF-BETA_1; 1.
 DR Growth factor; Mitogen; Glycoprotein.
 FT NON_TER
 FT PROPEP
 FT CHAIN
 FT DISULFID
 FT DISULFID
 FT DISULFID
 FT DISULFID
 FT CARBOHYD
 FT CARBOHYD
 FT CARBOHYD
 FT NON_TER
 SQ SEQUENCE 361 AA; 41931 MW; 949930FA970A3FD3 CRC64;

Query Match 31.2%; Score 673.5; DB 13; Length 361;
 Best Local Similarity 40.4%; Pred. No. 3.7e-50;
 Matches 155; Conservative 54; Mismatches 116; Indels 59; Gaps 14;

QY 52 QILSKRLASPPSGDVPGP--LPEAVIALYNSTRDRAVGESEVPEPEPE-----ADYV 104
 DB 1 QILCKIKLSCP---EIVPEPEVSRDIIAIVNSTRDLQEKANERATCERQRTGEIYV 57

QY 105 AKGVTVLM--VESGNOIYDKRGPHSLYMLFNTSELREAVEPYLLSRAELRLRL- 160
 DB 58 AKGVHRIIDMPFPAENVILPKHY-NPEFRRLRFDVSMEKNASN--LYVAELRIREFLQ 113
 QY 161 --KLKV-EQVVELYQ-----KYSNDSRWLYSNRLAASDSEWLSFDVTGYVRQMLRRE 212
 DB 114 NPKARVSEQRILELYQLIGHKDLTSPYQRYIDSKVVRRTGEWLSFDVTGEVSEWMLHRD 173
 QY 213 AIEGFRLSAHSS-----DSKNTLHVEINGFNSG--RQGLATL----HGMR 255
 DB 174 RNNGFISLHCPCCTIPVSNYIIPKSELEAFPAIDDSFVAGDLKMKRRHSQS 233
 QY 256 PELLNATPLERAQHLSRRRALDNTNSPYDVPDYASLALDNTNCFSSSTENKCCVROL 315
 DB 234 PHLLMLLPISYRLESQHS-HRQ-----KRALDAFCFRNVQDNCCLRSL 277
 QY 316 YIDFRKDLGKWKVHEPKGYHANFCLGCPGYIWSLDTQYSKVALYNQHNPGASAPCCVP 375
 DB 278 YIDFRKDLGKWKVHEPKGYHANFCLGCPGYIWSLDTQYSKVALYNQHNPGASAPCCVS 337

QY 376 QALEPLIYVYVGRKPKVEQLSNM 399
 DB 338 QDLEPLILYIKTKTKIRIQLSNM 361

RESULT 13
 002730 PRELIMINARY; PRT; 112 AA.
 AC 002730; 097501;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
 GN TGFb1 OR TGF-BETA-1.
 OS *Oryctolagus cuniculus* (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NC NCBL_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Taylor T.K., James E.R., McGonigle S., Yoho E.R.;
 RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RA Inoue K., Kawabe Y., Kodama T.;
 RL Submitted (Nov-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
 CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
 CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
 CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
 CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
 CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL: AF000133; AAB3806.1; -
 DR EMBL: AB020217; BAA36950.1; -
 DR HSSP: P01137; IRLA.
 DR InterPro: IPR002400; GF.cysknob.
 DR InterPro: IPR001839; TGFb.
 DR Pfam: PF00019; TGF-beta; 1.
 DR PRINTS: PR00438; GFCTSKNOT.
 DR ProDom: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF-BETA_1; 1.
 DR Growth factor; Mitogen; Glycoprotein.
 FT NON_TER
 FT CHAIN
 FT DISULFID
 FT DISULFID
 FT DISULFID
 FT DISULFID
 FT DISULFID
 FT DISULFID
 FT DISULFID
 FT CONFLICT
 TRANSFORMING GROWTH FACTOR BETA 1.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 INTERCHAIN (BY SIMILARITY).
 LD -> FS (IN REF. 2).

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FT CONFLICT 85 92 PULPIVYV -> ATAHRTTL (IN REF. 2).
SQ SEQUENCE 112 AA: 12795 MW: 53CSB7D6355A63 CRC64;
Query Match 29.6%; Score 638; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 8.4e-48;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 296 ADDTWCFSTENCCVROLYIDFRKLGWKWHEPKGYHANFCLGPPCPYIWSLDTQYSK 355
DB 1 ADDTWCFSTENCCVROLYIDFRKLGWKWHEPKGYHANFCLGPPCPYIWSLDTQYSK 60
QY 356 VVALYVQNHQHPGSAAPCCVQALPELPYVYVGRKPKVEQLSNMIVRSCKS 407
DB 61 VVALYVQNHQHPGSAAPCCVQALPELPYVYVGRKPKVEQLSNMIVRSCKS 112
RESULT 14
Q921T1 PRELIMINARY; PRT; 255 AA.
AC Q921T1
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Similar to transforming growth factor, beta 2.
GN TGFb2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL: BC011055; AAI11055.1; -.
MGD: MGI:96726; Tgfb2.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR ProSITE: PS00250; TGF_BETA_1; UNKNOWN_1.
DR GlycoProtein.
KW GLYCOPROTEIN.
SQ SEQUENCE 255 AA: 29087 MW: 94540017F3C5C219 CRC64;
Query Match 27.8%; Score 600; DB 11; Length 255;
Best Local Similarity 44.2%; Pred. No. 5.4e-44;
Matches 119; Conservative 42; Mismatches 68; Indels 40; Gaps 6;
QY 163 KYEQ--HVELYQK--YSNDSWRYLSNRLAPSDSPFWLSFDVTGVVROWLTRREALTEGR 218
DB 3 RVEATHVQILKSKDLSPQRYIDSKVYKTRAGEWLSFDVDAVQEWLHKKDRNLGFK 62
QY 219 LSAHSS-----DSKDNTHVE---INGFNSGRCDLATIHGMNR-----PFL 258
DB 63 ISLHPCCTFPVPSNNYIIPKSELEAFAGIDGTSTYASGDQKTIKSTRKKTSGKTPHL 122
QY 259 LMATPLERAQHLHSSRRRLDNTSYRVDVYASLADTNYCFSTENCCVROLYID 318
DB 123 LMLLPSTYRLSEQOSSRRKR-----ALDAAYCFRNVDNCCIRPLIYID 166
QY 319 FRKDLGKWIHEPKGYHANFCLGPPYIWSLDTQYSKVVALYVQNHQHPGSAAPCCVQAL 378
DB 167 FRKDLGKWIHEPKGYHANFCLGPPYIWSLDTQYSKVVALYVQNHQHPGSAAPCCVQAL 226
QY 379 EPLPIYVYVGRKPKVEQLSNMIVRSCKS 407
DB 227 EPLPIYVYVGRKPKVEQLSNMIVRSCKS 255
RESULT 15
Q9TV08 PRELIMINARY; PRT; 127 AA.

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AC Q9TV08;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Transforming growth factor beta-1 (fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID:9615;
RN [1]
RP SEQUENCE FROM N.A.
RA German A.J., Helps C.R., Hall E.J., Day M.J.;
RT "Cloning and sequencing of canine transforming growth factor beta 1
RT mRNA."
RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF091135; AAD46993.1; -.
DR HSSP: P01137; 1KLA.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00688; TGFb_propeptide; 1.
FT NON_TER 1
FT NON_TER 127
SQ SEQUENCE 127 AA: 14641 MW: D46D24ECA89F58DE CRC64;
Query Match 27.1%; Score 584.5; DB 6; Length 127;
Best Local Similarity 77.8%; Pred. No. 4.4e-43;
Matches 112; Conservative 5; Mismatches 10; Indels 17; Gaps 1;
QY 179 WRYSNRLAPSDSPFWLSFDVTGVVROWLTRREALTEGFRLSAHSSSDSKDNTHLVEING 238
DB 1 WRYSNRLAPSDSPFWLSFDVTGVVROWLSHGVEYEGFRLSAHSCSDSKDNTHLVDING 60
QY 239 FNSGRGDLATIHGMNRPELLMATPLERAQHLHSSRRRLDNTSYRVDVYASLALD 298
DB 61 FSSRRGDLATIHGMNRPELLMATPLERAQHLHSSRR-----ALD 103
QY 299 TNYCFSTENCCVROLYIDPRKD 322
DB 104 TNYCFSTENCCVROLYIDPRKD 127

```

Search completed: April 15, 2003, 12:00:28
Job time : 83 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:58:03 ; Search time 21 Seconds
(without alignments)

803.851 Million cell updates/sec

Title: US-10-017-372E-37

Sequence: 1 MAPSGRLPLPLPLMLLV.....GRPKVEQLSMYRSCKCS 407

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2030.5	94.0	390	1	TGFI_PIG
2	1929.5	89.4	390	1	TGFI_SHEEP
3	1916.5	88.8	390	1	TGFI_HUMAN
4	1914.5	88.7	390	1	TGFI_CERAT
5	1893.5	87.7	390	1	TGFI_CANFA
6	1839.5	85.2	390	1	TGFI_HORSE
7	1835.5	85.0	390	1	TGFI_MOUSE
8	1826.5	84.6	390	1	TGFI_CAVPO
9	1826.5	84.6	390	1	TGFI_BOVIN
10	1572.5	72.8	315	1	TGFI_CHICK
11	1047	48.5	373	1	TGFI_XENLA
12	868.5	40.2	382	1	TGFI_XENLA
13	852.5	39.5	412	1	TGFI_CHICK
14	834	38.6	409	1	TGFI_PIG
15	827.5	38.3	410	1	TGFI_MOUSE
16	826.5	38.3	412	1	TGFI_MOUSE
17	824.5	38.2	414	1	TGFI_HUMAN
18	824	38.2	414	1	TGFI_MOUSE
19	809	37.5	414	1	TGFI_HUMAN
20	808.5	37.4	413	1	TGFI_XENLA
21	808	37.4	412	1	TGFI_CHICK
22	805	37.3	435	1	TGFI_PIG
23	805	37.3	442	1	TGFI_RAT
24	482	22.3	112	1	TGFI_BOVIN
25	323.5	15.0	375	1	GDF8_MEIGA
26	321.5	14.9	375	1	GDF8_CHICK
27	311.5	14.4	375	1	GDF8_PIG
28	310.5	14.4	375	1	GDF8_PAPHA
29	308.5	14.3	375	1	GDF8_RAT
30	307.5	14.2	376	1	GDF8_HUMAN
31	306.5	14.2	376	1	GDF8_MOUSE
32	305.5	14.2	375	1	GDF8_SHEEP
33	300	13.9	405	1	GDF8_MOUSE

34	300	13.9	407	1	GDF8_HUMAN	O95390 homo sapien
35	296.5	13.7	375	1	GDF8_BOVIN	O18836 bos taurus
36	280.5	13.0	374	1	GDF8_BRARE	O42222 brachydanio
37	278.5	12.9	345	1	GDF8_RAT	O92217 ratius norv
38	275	12.7	425	1	IHBA_SHEEP	P43032 ovis aries
39	272.5	12.6	424	1	IHBA_PIG	P03970 sus scrofa
40	270.5	12.5	424	1	IHBA_MOUSE	O04958 mus musculu
41	270.5	12.5	424	1	IHBA_RAT	P18331 ratius norv
42	270.5	12.5	425	1	IHBA_BOVIN	P07995 bos taurus
43	269.5	12.5	426	1	IHBA_HORSE	P55102 equus cabal
44	268.5	12.4	426	1	IHBA_HUMAN	P08476 homo sapien
45	265.5	12.3	424	1	IHBA_CHICK	P27092 gallus gall

ALIGNMENTS

RESULT 1
TGFI_PIG STANDARD; PRT; 390 AA.
AC P07200: P08832:
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN TGFBI.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_Taxid=9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=87174844; PubMed=3470708;
RA Derynck R., Rhee L.;
RL "Sequence of the porcine transforming growth factor-beta precursor.";
RL Nucleic Acids Res. 15:3187-3187(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Miniature swine;
RX MEDLINE=89054010; PubMed=2461367;
RA Kondalajah P., van Obberghen-Schilling E., Ludwig R.L., Dhar R.,
RA Sporn M.B., Roberts A.B.;
RT "cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
RT Evidence for alternate splicing and polyadenylation.";
RT J. Biol. Chem. 263:18313-18317(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88335639; PubMed=3166520;
RA Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
RT "Nucleotide sequence of chicken transforming growth factor-beta 1
RT (TGF-beta 1).";
RL Nucleic Acids Res. 16:8730-8730(1988).
RN [4]
RP SHOWS THAT REF. 3 SEQUENCE IS FROM PIG.
RA Jakowlew S.B.;
RL Unpublished observations (MAR-1996).
RN [5]
RP SEQUENCE OF 279-322.
RX MEDLINE=87102890; PubMed=2879635;
RA Chelifer S., Weatherbee J.A., Tsang M.L.S., Anderson J.K., Mole J.E.,
RA Lucas R., Massague J.;
RL "The transforming growth factor-beta system, a complex pattern of
RL cross-reactive ligands and receptors.";
RL Cell 48:409-415(1987).
RN [6]
RP FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
RP PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
RP TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
RP HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
RP ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
RP A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
RN [7]
RP SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
RN [8]
RP SUBCELLULAR LOCATION: secreted.

FT	PROPEP	24	278	POTE
FT	CHAIN	279	390	TRAN

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FT DISULFID 285 294 BY SIMILARITY.
FT DISULFID 293 356 BY SIMILARITY.
FT DISULFID 322 387 BY SIMILARITY.
FT DISULFID 326 389 BY SIMILARITY.
FT DISULFID 355 355 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 244 246 CELL ATTACHMENT SITE (POTENTIAL).
SQ SEQUENCE 390 AA: 44291 MW: 10247299484DOE57 CMC64;

Query Match 89.4%; Score 1929.5; DB 1; Length 390;
Best Local Similarity 89.7%; Pred. No. 4,1e-147;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAVSGRLPLPLPLPLMLVLTGPGPAAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
DB 1 MPESGLRPLPLPLPLMLTLPSPVAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
QY 61 SPSPGQVPPGRLPEAVLATYNSTRDRVAGSEVPEPEADYKYKEYTVRLMVEGNCI 120
DB 61 SPSPGQVPPGRLPEAVLATYNSTRDRVAGSEVPEPEADYKYKEYTVRLMVEGNCI 120
QY 121 YDKRKGTPHSLYMLNTSELREAVPEVLLSRRAELRLRLKLVQHVHLYKYNSDSMR 180
DB 121 YDKMKSSHSIYMEFNSELREAVPEVLLSRADYRLRLKLVQHVHLYKYNSDSMR 180
QY 181 YLSKRLAPSPSPWELSDYGVYKQMTREAIKGFRLSAHSSDSKNTLHVELNGFN 240
DB 181 YLSKRLAPSPSPWELSDYGVYKQMTREAIKGFRLSAHSSDSKNTLHVELNGFN 240
QY 241 SGRGDLATIGMNRPFLLMATPLERAOHLHSSRRRLADNSPYDVPDASLALDIN 300
DB 241 SGRGDLATIGMNRPFLLMATPLERAOHLHSSRRRLADNSPYDVPDASLALDIN 300
QY 301 YCFSTEKNCCVROLYIDFRKDLGKWKIHPEKGYHANFCLGCPYIWSIDTOYSKYLALY 360
DB 301 YCFSTEKNCCVROLYIDFRKDLGKWKIHPEKGYHANFCLGCPYIWSIDTOYSKYLALY 360
QY 361 NQHPGASAPCCVQALEPLPIYVYVGRKPKVEOLSNMIVSCSCS 407
DB 361 NQHPGASAPCCVQALEPLPIYVYVGRKPKVEOLSNMIVSCSCS 407
QY 344 NQHPGASAPCCVQALEPLPIYVYVGRKPKVEOLSNMIVSCSCS 390
DB 344 NQHPGASAPCCVQALEPLPIYVYVGRKPKVEOLSNMIVSCSCS 390

RESULT 3
TCF1_HUMAN STANDARD: PRT: 390 AA.
AC P01137: Q9UCG4;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN TGFBI OR TGFBI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85296301; PubMed=3861940;
RA Derynck R., Jarrett J.A., Chen E.Y., van Tilburg A.,
RA Assoulin R.K., Roberts A.B., Sporn M.B., Goeddel D.V.;
RA "Human transforming growth factor-beta complementary DNA sequence and
RT expression in normal and transformed cells.";
RL Nature 316:701-705(1985).
RN [3]

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RP SEQUENCE FROM N.A.
RC TISSUE=Ductenun, and Eye;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 279-390 FROM N.A.
RC TISSUE=Carcinoma;
RA Urushizaki Y., Nitsui Y., Terui T., Koshida Y., Mahara K., Kohgo Y.,
RA Urushizaki I., Takahashi Y., Ito H.;
RT "Cloning and expression of the gene for human transforming growth
RT factor-beta in Escherichia coli.";
RL Tumor Res. 22:41-55(1987).
RN [5]
RP SEQUENCE OF 279-329.
RC TISSUE=Bladder carcinoma;
RA MEDLINE=93229900; PubMed=8471846;
RA Bourdrel L., Lin C.-H., Lauren S.L., Elmore R.H., Sugerman B.J.,
RA Hu S., Westcott K.R.;
RT "Recombinant human transforming growth factor-beta 1: expression by
RT Chinese hamster ovary cells, isolation, and characterization.";
RL Protein Expr. Purif. 4:130-140(1993).
RN [6]
RP SEQUENCE OF 279-301.
RA MEDLINE=85131019; PubMed=2982829;
RA Massague J., Like B.;
RT "Cellular receptors for type beta transforming growth factor. Ligand
RT binding and affinity labeling in human and rodent cell lines.";
RL J. Biol. Chem. 260:2636-2645(1985).
RN [7]
RP STRUCTURE BY NMR OF 279-390.
RA MEDLINE=93144319; PubMed=8424942;
RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Plez K.A.,
RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA Torchia D.A.;
RT "Transforming growth factor beta 1: NMR signal assignments of the
RT recombinant protein expressed and isotopically enriched using Chinese
RL hamster ovary cells.";
RL Biochemistry 32:1152-1163(1993).
RN [8]
RP STRUCTURE BY NMR OF 279-390.
RA MEDLINE=93144320; PubMed=8424943;
RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Plez K.A.,
RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA Torchia D.A.;
RT "Transforming growth factor beta 1: secondary structure as determined
RT by heteronuclear magnetic resonance spectroscopy.";
RL Biochemistry 32:1164-1171(1993).
RN [9]
RP STRUCTURE BY NMR OF 279-390.
RA MEDLINE=96266150; PubMed=8679613;
RA Hnick A.P., Archer S.J., Qian S.W., Roberts A.B., Sporn M.B.,
RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA Torchia D.A.;
RT "Transforming growth factor beta 1: three-dimensional structure in
RT solution and comparison with the X-ray structure of transforming
RT growth factor beta 2.";
RL Biochemistry 35:8517-8534(1996).
RN [10]
RP FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION,
RC DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
CC CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE
CC SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE
CC ACTION OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
CC POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL: X05839; CAA29283.1; -.
DR EMBL: X05840; CAA29283.1; JOINED.
DR EMBL: X05843; CAA29283.1; JOINED.
DR EMBL: X05844; CAA29283.1; JOINED.
DR EMBL: X05849; CAA29283.1; JOINED.
DR EMBL: X05850; CAA29283.1; JOINED.
DR EMBL: X02812; CAA26580.1; JOINED.
DR EMBL: X02812; CAA26580.1; ALT_SEQ.
DR EMBL: BC001180; AAH01180.1; -.
DR EMBL: BC000125; AAH00125.1; -.
DR EMBL: BC022242; AAH22242.1; -.
DR EMBL: M38449; AAA36735.1; -.
DR PIR: A01395; WEFU2.
DR PIR: A22290; A22290.
DR PIR: A27513; A27513.
DR PDB: 1KLA; 17-AUG-96.
DR PDB: 1KLC; 17-AUG-96.
DR PDB: 1KLD; 17-AUG-96.
DR Genew; HGNC:11766; TGFBI.
DR MIM: 190180; -.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR003911; TGF_TGFB.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR01423; TGFbeta.
DR PRODOM; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 23
FT PROPEP 24 278
FT CHAIN 279 390
FT DISULFID 285 294
FT DISULFID 293 356
FT DISULFID 322 387
FT DISULFID 326 389
FT DISULFID 355 355
FT CARBOHYD 82 82
FT CARBOHYD 136 136
FT CARBOHYD 176 176
FT SITE 244 246
FT CONFLICT 10 10
FT CONFLICT 159 159
SQ SEQUENCE 390 AA; 44341 MW; 753916142502886E CRC64;

Query Match 88.8%; Score 1916.5; DB 1; Length 390;
Best Local Similarity 89.7%; Pred. No. 4.5e-146;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

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OY 301 YCFSSTEKNCVQOLYIDFRKDLGKKWIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 360
DB 284 YCFSSTEKNCVQOLYIDFRKDLGKKWIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 343
OY 361 NOHNGASAPCCVPQALEPLIVYVGRKPKVEQLSNMIVRSCKKS 407
DB 344 NOHNGASAPCCVPQALEPLIVYVGRKPKVEQLSNMIVRSCKKS 390

RESULT 4
TGF1_CERAE
ID TGF1_CERAE STANDARD: PRT; 390 AA.
AC P09533;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN TGFBI.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87246074; Pubmed=3474130;
RA Sharples K., Plozman G.D., Rose T.M., Twardzik D.R., Purchio A.F.;
RT "Cloning and sequence analysis of simian transforming growth
factor-beta cDNA."
RL DNA 6:239-244(1987).
CC -1- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROL PROLIFERATION,
CC DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
CC CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM HAVE
CC SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATE THE
CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
CC POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/
CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL: M16658; AAA35369.1; -.
DR PIR: A26960; A26960.
DR HSSP; P01137; 1KLA.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR003911; TGF_TGFB.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR01423; TGFbeta.
DR PRODOM; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 16
FT PROPEP 17 278
FT CHAIN 279 390
FT DISULFID 285 294
FT DISULFID 293 356
FT DISULFID 322 387
FT DISULFID 326 389
FT DISULFID 355 355
FT CARBOHYD 82 82
FT CARBOHYD 136 136

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FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SITE 244 246 CELL ATTACHMENT SITE (POTENTIAL).
 SQ SEQUENCE 390 AA: DEF63E2BAB44320E CMC64;

Query Match 88.7%; Score 1914.5; DB 1; Length 390;
 Best Local Similarity 89.4%; Pred. No. 6.5e-146;
 Matches 364; Conservative 10; Mismatches 16; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLPLMLVLTTPGPRAGLSTCKTIDMEIVKRRRIEIRGOILSKRLA 60
 DB 1 MPBSGLPLPLPLPLMLVLTTPSRPAGLSTCKTIDMEIVKRRRIETRGQILSKRLA 60
 QY 61 SPSPQGVPPGPEPLPEAVLALYNSTRDVRAGESVEPEPEADYAKETRYLVAVESGNOI 120
 DB 61 SPSPQGVPPGPEPLPEAVLALYNSTRDVRAGESVEPEPEADYAKETRYLVAVESGNOI 120
 QY 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRALRLRLKIKVQHVLYOKYSNDSWR 180
 DB 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRALRLRLKIKVQHVLYOKYSNDSWR 180
 QY 181 YLSNRLLAPSPSPPELSDVYGVVROWLITRREALTGFRLSAHSDDSKONTLHVEINGFN 240
 DB 181 YLSNRLLAPSPSPPELSDVYGVVROWLITRREALTGFRLSAHSDDSKONTLHVEINGFN 240
 QY 241 SGRSGDLATIGHMNRPELLMATPLERAQHLHSSRRRALDNTSYDYVDYASIALDTN 300
 DB 241 TGRGDLATIGHMNRPELLMATPLERAQHLHSSRRRALDNTSYDYVDYASIALDTN 300
 QY 301 YCFSSSTERNCCVROLYIDFRKDLGKMWIHEPKGYANFLGCPPIYWSLDTQYSKYLALY 360
 DB 284 YCFSSSTERNCCVROLYIDFRKDLGKMWIHEPKGYANFLGCPPIYWSLDTQYSKYLALY 343
 QY 361 NONHNGASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVSCSCS 407
 DB 344 NONHNGASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVSCSCS 390

RESULT 5
 TGFL_CANFA
 ID TGFL_CANFA STANDARD: PRT: 390 AA.

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 CN TGB1.
 OS Canis familiaris (dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Jugular vein endothelial;
 RX MEDLINE=95237630; PubMed=7721110;
 RA Manning A.M., Auchampack J.A., Diong R.F., Slightom J.L.;
 RA "Cloning of a canine cDNA homologous to the human transforming growth
 factor-beta 1-encoding gene.";
 RL Gene 155:307-308(1995).
 CC -1- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
 PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
 TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
 HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
 ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
 A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC -1- SUBUNIT: HOMODIMER. DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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DR EMBL: I34956; AAA51458.1; -
 DR HSSP: P01137; IKLA
 DR InterPro: IPR002400; GF_cysknob.
 DR InterPro: IPR003911; TGF_TGFD.
 DR InterPro: IPR001839; TGFB.
 DR InterPro: IPR001111; TGFB.N.
 DR Pfam: PR000688; TGF-beta; 1.
 DR Pfam: PR006688; TGF-beta; 1.
 DR PRINTS: PR00438; GFCISKNOT.
 DR PRINTS: PR01423; TGFBETA.
 DR ProDom: PD000357; TGFB.
 DR SMART: SM00204; TGFB; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 KW Growth factor; Mitogen; Glycoprotein; Signal.
 FT SIGNAL 1 23
 FT PROPEP 24 278
 FT CHAIN 279 390
 FT DISULFID 285 294
 FT DISULFID 293 356
 FT DISULFID 322 387
 FT DISULFID 326 389
 FT DISULFID 355 355
 FT CARBOHYD 82 82
 FT CARBOHYD 136 136
 FT CARBOHYD 176 176
 FT SITE 244 246
 SQ SEQUENCE 390 AA: 44185 MW: 84780EB8B7590E CMC64;

Query Match 87.7%; Score 1893.5; DB 1; Length 390;
 Best Local Similarity 88.7%; Pred. No. 3.1e-144;
 Matches 361; Conservative 12; Mismatches 17; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLPLMLVLTTPGPRAGLSTCKTIDMEIVKRRRIEIRGOILSKRLA 60
 DB 1 MPBSGLPLPLPLPLMLVLTTPSRPAGLSTCKTIDMEIVKRRRIETRGQILSKRLA 60
 QY 61 SPSPQGVPPGPEPLPEAVLALYNSTRDVRAGESVEPEPEADYAKETRYLVAVESGNOI 120
 DB 61 SPSPQGVPPGPEPLPEAVLALYNSTRDVRAGESVEPEPEADYAKETRYLVAVESGNOI 120
 QY 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRALRLRLKIKVQHVLYOKYSNDSWR 180
 DB 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRALRLRLKIKVQHVLYOKYSNDSWR 180
 QY 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRALRLRLKIKVQHVLYOKYSNDSWR 180
 DB 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRALRLRLKIKVQHVLYOKYSNDSWR 180
 QY 181 YLSNRLLAPSPSPPELSDVYGVVROWLITRREALTGFRLSAHSDDSKONTLHVEINGFN 240
 DB 181 YLSNRLLAPSPSPPELSDVYGVVROWLITRREALTGFRLSAHSDDSKONTLHVEINGFN 240
 QY 241 SGRSGDLATIGHMNRPELLMATPLERAQHLHSSRRRALDNTSYDYVDYASIALDTN 300
 DB 241 SGRSGDLATIGHMNRPELLMATPLERAQHLHSSRRRALDNTSYDYVDYASIALDTN 300
 QY 301 YCFSSSTERNCCVROLYIDFRKDLGKMWIHEPKGYANFLGCPPIYWSLDTQYSKYLALY 360
 DB 284 YCFSSSTERNCCVROLYIDFRKDLGKMWIHEPKGYANFLGCPPIYWSLDTQYSKYLALY 343
 QY 361 NONHNGASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVSCSCS 407
 DB 344 NONHNGASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVSCSCS 390
 RESULT 6
 TGFL_HORSE
 ID TGFL_HORSE STANDARD: PRT: 390 AA.
 AC 019011;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 CN TGB1.

```

OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RC MEDLINE=98185507; PubMed=9524819;
RA Penha-Goncalves M.N., Onions D.E., Nicolson L.;
RT "Cloning and sequencing of equine transforming growth factor-beta 1
RT (TGF-beta-1) cDNA.";
RL DNA Seq. 7:375-378(1997).
CC -I- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -I- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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DR EMBL: X99438; CAA67801.1; -
DR HSSP: P01137; IKLA.
DR InterPro: IPR002400; GE_cysknot.
DR InterPro: IPR003911; TGF_TGFP.
DR InterPro: IPR001839; TGFB.
DR InterPro: IPR001111; TGFB.N.
DR Pfam: PF000019; TGF-beta; 1.
DR Pfam: PF00668; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR01423; TGFbeta.
DR PRODOM: PD000357; TGFBETA.
DR SMART: SM00204; TGFB; 1.
DR PROSITE: PS00250; TGF-BETA; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 278 BY SIMILARITY.
FT CHAIN 279 390 TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID 285 294 BY SIMILARITY.
FT DISULFID 293 356 BY SIMILARITY.
FT DISULFID 322 387 BY SIMILARITY.
FT DISULFID 326 389 BY SIMILARITY.
FT DISULFID 335 353 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 390 AA; 43974 MW; A86D15H44549691 CRC64;
Query Match 85.28; Score 1839.5; DB 1; Length 390;
Best Local Similarity 86.58; Pred. No. 6.6e-140;
Matches 352; Conservative 12; Mismatches 26; Indels 17; Gaps 1;
1 MAPSGRLPLPLPLMLVLTGPRPAAGSTCKTIDMEIVKRRRIEMIRGOILSLRLA 60
1 MPSPGRLPLPLPLMLVLTGPRPAAGSTCKTIDMEIVKRRRIEMIRGOILSLRLA 60
61 SPSPQGVDPPEPLPEAVLALYNSTRDVAGSEVPEPEADYAKETRVLMVESGNOI 120
61 SPSPQGVDPPEPLPEAVLALYNSTRDVAGSEVPEPEADYAKETRVLMVESGNOI 120
61 SPSPQGVDPPEPLPEAVLALYNSTRDVAGSEVPEPEADYAKETRVLMVESGNOI 120
121 YKFKCTPHSLVLMFNTSELRVAPEVYLLSRALRLRLKIKVEQHVLYOKYSNDSR 180
121 YKFKCTPHSLVLMFNTSELRVAPEVYLLSRALRLRLKIKVEQHVLYOKYSNDSR 180
121 YKFKCTPHSLVLMFNTSELRVAPEVYLLSRALRLRLKIKVEQHVLYOKYSNDSR 180
121 YKFKCTPHSLVLMFNTSELRVAPEVYLLSRALRLRLKIKVEQHVLYOKYSNDSR 180

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QY 181 YLSNRLAPSDSPENLSPDYVTGVVROWLTPRRAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
QY 181 YLSNRLAPSDSPENLSPDYVTGVVROWLTPRRAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
DB 181 YLSNRLAPSDSPENLSPDYVTGVVROWLTPRRAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
QY 241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLSSRRRLADLTNSPYDVPDYASLADTN 300
DB 241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLSSRRRLADLTNSPYDVPDYASLADTN 300
QY 301 YCFSTERNKCCVROLYIDPRKDLGKWHIEPKRYHANFCGPGPYTMSLDTQYSKVLYAL 360
DB 284 YCFSTERNKCCVROLYIDPRKDLGKWHIEPKRYHANFCGPGPYTMSLDTQYSKVLYAL 360
QY 361 NQHNNGASAPCCVQVLEPLPIVYVGRKPKVEQSLNMTIVRSCKS 407
DB 344 NQHNNGASAPCCVQVLEPLPIVYVGRKPKVEQSLNMTIVRSCKS 390
RESULT 7
TGF_MOUSE STANDARD; PRT; 390 AA.
ID TGF_MOUSE
AC P04202;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN TGFBI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86168129; PubMed=3007454;
RA Derynck R., Jarrett J.A., Chen E.Y., Goeddel D.V.;
RT "The murine transforming growth factor-beta precursor.";
RL J. Biol. Chem. 261:4377-4379(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=96096545; PubMed=8522200;
RA Guron C., Sudarshan C., Raghow R.;
RT "Molecular organization of the gene encoding murine transforming
RT growth factor-beta 1.";
RL Gene 165:325-326(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6, and NOD/Lt; TISSUE=Spleen;
RA Polrot L., Benoist C., Mathis D.;
RT "Transforming growth factor-beta 1 sequence and expression: no
RT difference between NOD/Lt and C57BL/6 mouse strains.";
RL Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.
CC -I- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -I- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC or send an email to license@isb-sib.ch).
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DR EMBL: M13177; AAA40423.1; -
DR EMBL: L42462; AAB00138.1; -
DR EMBL: L42456; AAB00138.1; JOINED.
DR EMBL: L42457; AAB00138.1; JOINED.

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DR EMBL: L42458; AAB00138.1; JOINED.
DR EMBL: L42459; AAB00138.1; JOINED.
DR EMBL: L42460; AAB00138.1; JOINED.
DR EMBL: L42461; AAB00138.1; JOINED.
DR EMBL: A0009862; CAA008900.1; -.
DR PIR: A01396; MFM52.
DR HSSP: P01137; 1KLA.
DR MGD: MGI:98725; Tgfbl.
DR InterPro: IPR002400; GF_cysknott.
DR InterPro: IPR003911; TGF_TGFP.
DR InterPro: IPR001839; TGFB.
DR InterPro: IPR001111; TGFB.N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFB_propeptide; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR01423; TGFBETA.
DR PRODOM: PD000357; TGFB; 1.
DR SMART: SM00204; TGFB; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
DR Growth factor; Mitogen; Glycoprotein; signal.
FT SIGNAL 1 23
FT PROPEP 24 278
FT CHAIN 279 390
FT DISULFID 283 294
FT DISULFID 293 356
FT DISULFID 322 387
FT DISULFID 326 389
FT DISULFID 355 355
FT CARBOHYD 82 82
FT CARBOHYD 136 136
FT CARBOHYD 176 176
FT SITE 244 246
SQ SEQUENCE 390 AA; 44310 MW; 4381A51B71D689E CRC64;

Query Match 85.0%; Score 1835.5; DB 1; Length 390;
Best Local Similarity 85.0%; Pred. No. 1.4e-139;
Matches 346; Conservative 15; Mismatches 29; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLPLMLVLVTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
DB 1 MPBSGLRLPLPLPLPLMLVLVTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
QY 61 SPSQGVPPGPPLEAVLALYNSTRDVAGSVEPEPEADYAKETRYLVAVESGNOI 120
DB 61 SPSQGVPPGPPLEAVLALYNSTRDVAGSADPEPEADYAKETRYLVAVDRNNAI 120
QY 121 YDKKGTPIHSIYMFNSELREAVPEPVLISRAELRLKLIKVOHVELYKYSNDSMR 180
DB 121 YDKKGTPIHSIYMFNSELREAVPEPVLISRAELRLKLIKVOHVELYKYSNDSMR 180
QY 121 YDKKGTPIHSIYMFNSELREAVPEPVLISRAELRLKLIKVOHVELYKYSNDSMR 180
DB 121 YDKKGTPIHSIYMFNSELREAVPEPVLISRAELRLKLIKVOHVELYKYSNDSMR 180
QY 241 SGRGGDLATIHGNNRPPELLMLATPLERAQHLHSSRRRALDINSYVDVAYASALDIN 300
DB 241 SGRGGDLATIHGNNRPPELLMLATPLERAQHLHSSRRRALDINSYVDVAYASALDIN 300
QY 241 PKRGDGLTIDHNNRPPELLMLATPLERAQHLHSSRRRALDINSYVDVAYASALDIN 300
DB 241 PKRGDGLTIDHNNRPPELLMLATPLERAQHLHSSRRRALDINSYVDVAYASALDIN 300
QY 301 YCFSTENKCCVROLYIDFRKDLGKWKIHERKGYHANFCLGCPYIWSIDTOYSKVLALY 360
DB 301 YCFSTENKCCVROLYIDFRKDLGKWKIHERKGYHANFCLGCPYIWSIDTOYSKVLALY 360
QY 284 YCFSTENKCCVROLYIDFRKDLGKWKIHERKGYHANFCLGCPYIWSIDTOYSKVLALY 343
DB 284 YCFSTENKCCVROLYIDFRKDLGKWKIHERKGYHANFCLGCPYIWSIDTOYSKVLALY 343
QY 361 NQHPNGASAPCVPAOLEPLIYVYVGRPKVEQLSNMIVSCSCS 407
DB 361 NQHPNGASAPCVPAOLEPLIYVYVGRPKVEQLSNMIVSCSCS 407
QY 344 NQHPNGASAPCVPAOLEPLIYVYVGRPKVEQLSNMIVSCSCS 390
DB 344 NQHPNGASAPCVPAOLEPLIYVYVGRPKVEQLSNMIVSCSCS 390

RESULT 8
TGFL_RAT STANDARD: PRT: 390 AA.
AC P17246;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN TGFbl.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE-Heart;
RX MEDLINE=90272425; PubMed=2349108;
RA Qian S.W., Kondalish P., Roberts A.B., Sporn M.B.;
RT cDNA cloning by PCR of rat transforming growth factor beta-1.;
RL Nucleic Acids Res. 18:3059-3059(1990).
CC -1- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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DR EMBL: X52498; CAA36741.1; -.
DR PIR: S10219; S10219.
DR HSSP: P01137; 1KLA.
DR InterPro: IPR002400; GF_cysknott.
DR InterPro: IPR003911; TGF_TGFB.
DR InterPro: IPR001839; TGFB.
DR InterPro: IPR001111; TGFB.N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFB_propeptide; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR01423; TGFBETA.
DR PRODOM: PD000357; TGFB; 1.
DR SMART: SM00204; TGFB; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
DR Growth factor; Mitogen; Glycoprotein; signal.
FT SIGNAL 1 23
FT PROPEP 24 278
FT CHAIN 279 390
FT DISULFID 283 294
FT DISULFID 293 356
FT DISULFID 322 387
FT DISULFID 326 389
FT DISULFID 355 355
FT CARBOHYD 82 82
FT CARBOHYD 136 136
FT CARBOHYD 176 176
FT SITE 244 246
SQ SEQUENCE 390 AA; 44329 MW; 5E21108ED50D853C CRC64;

Query Match 85.0%; Score 1835.5; DB 1; Length 390;
Best Local Similarity 85.0%; Pred. No. 1.4e-139;
Matches 346; Conservative 14; Mismatches 30; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLPLMLVLVTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
DB 1 MPBSGLRLPLPLPLPLMLVLVTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
QY 61 SPSQGVPPGPPLEAVLALYNSTRDVAGSVEPEPEADYAKETRYLVAVESGNOI 120
DB 61 SPSQGVPPGPPLEAVLALYNSTRDVAGSADPEPEADYAKETRYLVAVDRNNAI 120

[illegible][illegible]

RESULT	10
DT	DT
AC	AC
DT	01-NOV-1990 (Rel. 16, Created)
DT	01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1) (Fragment).
 OS TGFBI.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=91042552; PubMed=3153459;
 RA van Obberghen-Schilling E., Kondalish P., Ludwig R.L., Sporn M.B.,
 RA Baker C.C.;
 RT "Complementary deoxyribonucleic acid cloning of bovine transforming
 RT growth factor-beta 1";
 RL Mol. Endocrinol. 1:693-698(1987).
 RN [2]
 RN SUBUNITS.
 RC TISSUE=Bone;
 RX MEDLINE=92129307; PubMed=1733936;
 RA Ogawa Y., Schmidt D.K., Dasch J.R., Chang R.J., Glaser C.B.;
 RT "Purification and characterization of transforming growth factor-beta
 RT 2.3 and -beta 1.2 heterodimers from bovine bone.";
 RL J. Biol. Chem. 267:2325-2328(1992).
 CC -1- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
 CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
 CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
 CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
 CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
 CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC -1- SUBUNIT: HOMODIMER. DISULFIDE-LINKED. HETERODIMERS OF TGF-BETA 1/2
 CC HAVE BEEN FOUND IN BONE.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL; M36271; AAA30778.1; -;
 DR PIR; A40057; A40057.
 DR HSSP: P01137; 1KLA.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb_N.
 DR Pfam: PF000688; TGFb_propeptide; 1.
 DR ProDom: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 KW Growth factor; Mitogen; Glycoprotein.
 KM
 FT NON_TER 1
 FT PROPEP 1 203
 FT CHAIN 204 315 TRANSFORMING GROWTH FACTOR BETA 1.
 FT DISULFID 210 219 BY SIMILARITY.
 FT DISULFID 218 281 HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
 FT DISULFID 247 312 BY SIMILARITY.
 FT DISULFID 251 314 BY SIMILARITY.
 FT DISULFID 280 280 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 169 171 CELL ATTACHMENT SITE (POTENTIAL).
 SQ SEQUENCE 315 AA; 36269 MW; C217A23D994E00E CRC64;
 Query Match 72.8%; Score 1572.5; DB 1; Length 315;
 Best Local Similarity 88.9%; Pred. No. 1.2e-118;
 Matches 295; Conservative 9; Mismatches 11; Indels 17; Gaps 1;
 OY 76 AVLAALYNSTRDRAVAGSAPPEPEADYAKETRYALWVESGNQIYDKRKGTPHSLMLF 135

DB 1 ALAALYNSTRDRAVAGSAPPEPEADYAKETRYALWVESGNKIYDKMKSSSHSIYMF 60
 OY 136 NSELREAVPEPILLSRAELRLRLKIKYQHVHLYOKYNSDSRYSNRLAPSDSPW 195
 DB 61 NSELREAVPEPILLSRAELRLRLKIKYQHVHLYOKYNSDSRYSNRLAPSDSPW 120
 OY 196 LSPDYGVVROWLTLREAIIGFRLSAHSSSDSKDNTLHVEINGFNSGRGLATIHGMNR 255
 DB 121 LSPDYGVVROWLTLREAIIGFRLSAHSSSDSKDNTLHVEINGFNSGRGLATIHGMNR 180
 OY 256 PELLMATPLERAQHLLSHSRRLALDYNYPYDVAASLADITNCFSSTEKNCVROL 315
 DB 181 PELLMATPLERAQHLLSHSRRLALDYNYPYDVAASLADITNCFSSTEKNCVROL 223
 OY 316 YIDPRDLGKMKWIHEPGYANANCLGPCPYIWSIDTQYSKVALYNOHNPASAPCCVP 375
 DB 224 YIDPRDLGKMKWIHEPGYANANCLGPCPYIWSIDTQYSKVALYNOHNPASAPCCVP 283
 OY 376 QALEPLIYVYVGRKPKVEQLSMNIVRSCKS 407
 DB 284 QALEPLIYVYVGRKPKVEQLSMNIVRSCKS 315
 RESULT 11
 TGF1.CHICK STANDARD; PRT; 373 AA.
 ID TGF1.CHICK
 AC P09531;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1) (TGF-beta 4)
 DE (Fragment).
 GN TGFBI.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=White leghorn;
 RX MEDLINE=89112198; PubMed=2464131;
 RA Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
 RT "Complementary deoxyribonucleic acid cloning of a messenger
 RT ribonucleic acid encoding transforming growth factor beta 4 from
 RT chicken embryo chondrocytes.";
 RL Mol. Endocrinol. 2:1186-1195(1988).
 RN [2]
 RN REVISIONS.
 RX MEDLINE=92357039; PubMed=1333860;
 RA Burt D.W., Jakowlew S.B.;
 RT "Correction: a new interpretation of a chicken transforming growth
 RT factor-beta 4 complementary DNA.";
 RL Mol. Endocrinol. 6:989-992(1992).
 CC -1- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
 CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
 CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
 CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
 CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
 CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC -1- SUBUNIT: HOMODIMER. DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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Db 116 -----HEFKKFNASHRENVGMSLHHAELRMVKKOTDKNMQRMELFMKKYQENGTH 170
 QY 180 -RVLNRLAPSDSPWELSDYTGVRWLTTRRALEGFRLSAH---SSSDSKNTLHVE 235
 CC 171 SRYLESKYITPVDEDMWSEFDTKTVNEMLEKRAEENEFGLQAPACKCPPTPAKD----ID 226
 Db 236 INFNNSRRDDLATIHOM--NRPLLMATPLERAQHSHSRHRALDTNSPYVPVDPYA 293
 QY 227 IEGF-PALRDLNLSLSEKENTPYLMTSPAEKIDVTSSKKR----- 270
 Db 294 SLADLTNYCFSTSEKNCVRLQYIDFRKDLGKMKWHEPKGYHANCLGPCPYISLDTQY 353
 QY 271 --GVGQYCCGNNBNPCVRLYINFRDLGKMKWHEPKGYEANYCLGCPYIWMGMDTQY 328
 Db 354 SKVLTALYNQHNPGASAPCCVPOALEPLPIYVYGRKPKVQLSMYVRSCKS 407
 QY 329 SKVLTALYNQHNPGASAPCCVPOALEPLPIYVYGRKPKVQLSMYVRSCKS 382
 Db
 RESULT 13
 TGF3_CHICK STANDARD; PRT: 412 AA.
 ID TGF3_CHICK STANDARD; PRT: 412 AA.
 AC P16047;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 3 precursor (TGF-beta 3).
 GN TGFβ3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID-9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-9906966; PubMed-3211158;
 RA Jakowlew S.B., Dillard P.J., Kondiah P., Sporn M.B., Roberts A.B.;
 RT "Complementary deoxyribonucleic acid cloning of a novel transforming
 RT growth factor-beta messenger ribonucleic acid from chick embryo
 RT chondrocytes";
 RT Mol. Endocrinol. 2:747-755(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN-White leghorn;
 RC MEDLINE-95169270; PubMed-7865129;
 RA Burt D.W., Dey B.R., Paton I.R., Morrice D.R., Law A.S.;
 RT "The chicken transforming growth factor-beta 3 gene: genomic
 RT structure, transcriptional analysis, and chromosomal location.";
 RT DNA Cell Biol. 14:111-123(1995).
 RN [3]
 RP SEQUENCE OF 1-117 FROM N.A.
 RA STRAIN-White leghorn; TISSUE-Blood;
 RC MEDLINE-92134496; PubMed-1840616;
 RA Burt D.W., Dey B.R., Paton I.R.;
 RT "Comparative analysis of human and chicken transforming growth
 RT factor-beta 2 and -beta 3 promoters.";
 RT J. Mol. Endocrinol. 7:175-183(1991).
 RN [4]
 RP SEQUENCE OF 1-117 FROM N.A.
 RA MEDLINE-93024487; PubMed-1406706;
 RA Jakowlew S.B., Lechleider R., Geiser A.G., Kim S.J.,
 RA Santa-Coloma T.A., Cubert J., Sporn M.B., Roberts A.B.;
 RT "Identification and characterization of the chicken transforming
 RT growth factor-beta 3 promoter";
 RT Mol. Endocrinol. 6:1285-1298(1992).
 CC -1- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC -----
 CC EMBL: M31154; AAA49089.1; -;
 CC EMBL: X58127; CAA41128.2; -;
 CC EMBL: X60055; CAA41128.2; JOINED.
 CC EMBL: X60091; CAA41128.2; JOINED.
 CC EMBL: X60090; CAA41128.2; JOINED.
 CC EMBL: S46000; AAB23575.1; -;
 CC PIR: A34939; A34939.
 CC HSSP: P10600; ITGJ.
 CC InterPro: IPR003911; TGF-TGFB.
 CC InterPro: IPR001839; TGFB.
 CC InterPro: IPR001111; TGFB_N.
 CC Pfam: PF00019; TGF-beta; 1.
 CC Pfam: PF00688; TGF-beta-propeptide; 1.
 CC PRINTS: PR01423; TGF-beta.
 CC ProDom: PD000357; TGFB; 1.
 CC SMART: SM00204; TGFB; 1.
 CC SMART: SM00250; TGF-BETA_1; 1.
 CC PROSITE: PS00250; TGF-BETA_1; 1.
 CC Growth factor; Mitogen; Glycoprotein; Signal.
 CC KW SIGNAL
 CC FT PROPEP 24 300
 CC FT CHAIN 301 412
 CC FT DISULFID 307 316
 CC FT DISULFID 315 378
 CC FT DISULFID 344 409
 CC FT DISULFID 348 411
 CC FT DISULFID 377 377
 CC FT CARBOHYD 74 74
 CC FT CARBOHYD 135 135
 CC FT CARBOHYD 142 142
 CC FT SITE 261 263
 CC FT CONFLICT 323 326
 CC SQ SEQUENCE 412 AA; 47077 MW; 1CAB883170069D55 CMC64;
 Query Match 39.5%; Score 852.5; DB 1; Length 412;
 Best Local Similarity 45.5%; Pred. No. 7; 6e-61;
 Matches 195; Conservative 56; Mismatches 117; Indels 61; Gaps 14;
 QY 15 LMLVLTTPGPRAGLSTCKITIMELVLRKRLEIRGQILSKRLASPPSGDVPGRPLP 74
 Db 9 LVLTLSTFATVSLALSSCTLTDLHKKRVEALRGQLSKRLTSPPE--SVGAHP 66
 QY 75 EAVLALVSTDRVAGEVEPEPE-----PEADYAKVTRVLMVE--SGNQTIDKF 124
 Db 67 YQILALVNSTREL--EMEEKEKESCSQENTSEYVAKHFKPMIGQLPHEHNLGICP 124
 QY 125 KGPHTSLYMLFNTSELRAVEPEVLLSRAELRLRL---KUKVEQHEVLYKYSND--- 177
 Db 125 KGVASNVFR-FNVS--SAEKSTNLPFAEFVLRVPNPSKRSKEIDELFOLRDEHI 180
 QY 178 -SWRLNRLAPSDSPWELSDYTGVRWLTTRRALEGFRLSAH---SSSDSKND 229
 Db 181 AKORYLSGRNVQTRGSPWELSDYTGVRWLTTRRALEGFRLSAH---SSSDSKND 240
 QY 230 N---TLHVEINFGNG---RRGLDTI---HGMNRPFLMLMTPLERAQH--LHSSRHR 278
 Db 241 NIHEVLEIKFKGIDSEDDYGRGDLGRKKOKDLNHNHLLMLPRLRLSPLTGGGKRKR 300
 QY 279 ALDTNSYPDVDPVYASLADTNYCFSTSEKNCVRLQYIDFRKDLGKMKWHEPKGYHANF 338
 Db 301 -----ALDTNYCFSTSEKNCVRLQYIDFRKDLGKMKWHEPKGYHANF 343
 QY 339 CLGCPYIWSLDTQYSKVLTALYNQHNPGASAPCCVPOALEPLPIYVYGRKPKVQLSMYVRSCKS 398
 Db 344 CSGCPYIWSLDTQYSKVLTALYNQHNPGASAPCCVPOALEPLPIYVYGRKPKVQLSMYVRSCKS 403
 QY 399 MIVRSCKS 407
 Db 404 MIVRSCKS 412

```

RESULT 14
ID TGF3_PIG STANDARD: PRT: 409 AA.
AC P15203;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 3 precursor (TGF-beta 3).
GN TGFb3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ovary;
RX MEDLINE=69091120; PubMed=3208746;
RA Derynck R., Lindquist B., Lee A., Tamm J., Graycar J.L.,
RA Rhee L., Mason A.J., Miller D.A., Coffey R.J., Moses H.L.,
RA Chen E.Y.;
RT "A new type of transforming growth factor-beta, TGF-beta 3."
RL EMBL J. 7:3737-3743(1988)
CC -1- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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EMBL: X14150; CAA32363.1; -
PIR: S01825; S01825.
DR HSSP: P10600; ITGJ.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR003911; TGF_TGFB.
DR InterPro: IPR001839; TGFB.
DR InterPro: IPR001111; TGFB_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFB-Propeptide; 1.
DR PRINTS: PR00438; GFCSKNOT.
DR PRINTS: PR01423; TGFEBETA.
DR ProDom: PD000357; TGFB; 1.
DR SMART: SM00204; TGFB; 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 297
FT CHAIN 298 409 TRANSFORMING GROWTH FACTOR BETA 3.
FT DISULFID 304 313 BY SIMILARITY.
FT DISULFID 312 375 BY SIMILARITY.
FT DISULFID 341 406 BY SIMILARITY.
FT DISULFID 345 408 BY SIMILARITY.
FT DISULFID 374 408 INTERCHAIN (BY SIMILARITY).
FT CAROHD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 259 261 CELL ATTACHMENT SITE (POTENTIAL).
FT SEQUENCE 409 AA: 46814 MW: B4900235B5CC955E CRC64;
Query Match 38.6%; Score 834; DB 1; Length 409;
Best Local Similarity 44.6%; Pred. No. 2,3e-59;
Matches 190; Conservative 58; Mismatches 122; Indels 56; Gaps 14;
15 LMLVLVLPGRRAAGSTCKTIDMELVKRRIRAIQQLISKLRLASPPSGDVPVPGPLP 74
7 LVALLLNFAVYLSMSTCTTDFDIKRRKVAIRQILSKLRLTSPDPDSML--ANIP 64

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QY 75 EAVLALYNSTR---DRVAGESEV--PEPEADYIAKEVTRVLMV---ESGNQYIDKFKG 126
DB 65 TQVLDLYNSTRELLEVEBERGDDCTQENTSESYAAKEIKYFMDIQLEHNDLAVCPKG 124
QY 127 TPHSLYMLFNTSELREAVEPEVLLSRRELRLR-----KLKVEQHVLELYKYSND-----S 178
DB 125 ITSKIFR-FNVSVER-----NEINLFRAEFFVLYLMPNPSKRSRSEDRIELFQLOPDEHIAK 180
QY 179 WRYSNLRLIAPSDSPWLSFDVTGVYRWMLTRREAIEGFRISAH-----SSSDSKDN- 230
DB 181 QRYIDGKNLPTRGAAEWLSEFVDVTGVREWLIRRESNLGLEISTHPCHTPOPNDDIENI 240
QY 231 --THIVEINGFMS-----GRGDLATIGM--NRFLLMLAPLERAGH--LHSSNRRALD 281
DB 241 QEWETKFRGVDSDDPGRGDLGRLLKKKEHSPHLILMLIPPRLDNPGDGAORRRK-- 297
QY 282 TNSYPDVPDYASLADLTNYCFSTTEKNCCVROLYIDFRKDLGMKWHEPKGYANFCLG 341
DB 298 -----ALDTNYCFRNLEENCVRPLYLIDFRDLDGMKWHEPKGYANFCSCG 343
QY 342 PCPIYWSLDTQYSKYLALYNOHNPASAPCCVQALPEPLIYVYGRKPKVEQLSNMIV 401
DB 344 PCPIYRSADTTHSVGLYNTLNPEASAPCCVQDLEPLIYVYGRKAKVEQLSNMIV 403
QY 402 RSCCKS 407
DB 404 KSCCKS 409
-----
RESULT 15
ID TGF3_MOUSE STANDARD: PRT: 410 AA.
AC P17125;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 3 precursor (TGF-beta 3).
GN TGFb3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90190650; PubMed=2628730;
RA Miller D.A., Lee A., Matsui Y., Chen E.Y., Moses H.L., Derynck R.;
RT "Complementary DNA cloning of the murine transforming growth
RT factor-beta 3 (TGF beta 3) precursor and the comparative expression
RT of TGF beta 3 and TGF beta 1 messenger RNA in murine embryos and
RT adult tissues."
RL MOL. Endocrinol. 3:1926-1934(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91000714; PubMed=2206556;
RA Denhez F., Latyatis R., Kondalish P., Roberts A.B., Sporn M.B.;
RT "Cloning by polymerase chain reaction of a new mouse TGF-beta,
RT mTGF-beta 3."
RL Growth factors 3:139-146(1990).
CC -1- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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EMBL: M32745; AAA0422.1; -

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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:59:01 ; Search time 37 Seconds
(Without alignments)
1057.479 Million cell updates/sec

Title: US-10-017-372E-37

Perfect score: 2159

Sequence: 1 MAPSGRLPLPLPLMLLV.....GRKKVEQLSMIVRSCKCS 407

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2033.5	94.2	390	2 A27512	transforming growth
2	2002	92.7	391	2 S01413	transforming growth
3	1929.5	89.4	390	2 I46463	transforming growth
4	1916.5	88.8	390	1 WPHU2	transforming growth
5	1914.5	88.7	390	2 A26960	transforming growth
6	1893.5	85.0	390	2 JC4023	transforming growth
7	1835.5	85.0	390	1 WPM52	transforming growth
8	1835.5	85.0	390	2 S10219	transforming growth
9	1572.5	72.8	315	2 A40057	transforming growth
10	1047	48.5	373	2 A41918	transforming growth
11	871.5	40.4	382	2 A34939	transforming growth
12	868.5	40.2	412	2 B61036	transforming growth
13	834	38.6	409	2 S01825	transforming growth
14	827.5	38.3	410	2 A41397	transforming growth
15	826.5	38.3	410	2 A55706	transforming growth
16	824.5	38.2	414	2 A36169	transforming growth
17	824	38.2	414	1 WPM52	transforming growth
18	809	37.5	414	1 WPM52	transforming growth
19	809	37.5	414	2 A31249	transforming growth
20	808.5	37.4	413	1 WPM52	transforming growth
21	808	37.4	412	2 A39489	transforming growth
22	793	36.7	442	2 B31249	transforming growth
23	691.5	33.0	130	2 I48196	transforming growth
24	482	22.3	112	2 A61439	transforming growth
25	275	12.6	425	2 I47072	inhibin beta-A cha
26	272.5	12.5	424	1 WPM52	inhibin beta-A cha
27	270	12.5	424	1 S31440	inhibin beta-A cha
28	270	12.5	425	1 S50898	inhibin beta-A cha
29	268.5	12.4	426	1 B24248	inhibin beta-A cha

ALIGNMENTS

RESULT 1

A27512 transforming growth factor beta-1 precursor - pig

N:Alternate names: TGF-beta

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 05-Jun-1988 #sequence,revision 05-Jun-1988 #text_change 16-Jul-1999

C:Accession: A27512; A26356; I46557

R:Deruyck, R.; Rhee, L.

Nucleic Acids Res. 15, 3187, 1987

A:Title: Sequence of the porcine transforming growth factor-beta precursor.

A:Reference number: A27512; MUID:87174844; PMID:3470708

A:Accession: A27512

A:Molecule type: mRNA

A:Residues: 1-390 <CDR>

R:Chelitz, S.; Weathersee, J.A.; Tsang, M.L.S.; Anderson, J.K.; Mole, J.E.; Lucas, R.

Cell 48, 409-415, 1987

A:Title: The transforming growth factor-beta system, a complex pattern of cross-react

A:Reference number: A90890; MUID:87102890; PMID:2879635

A:Accession: A26356

A:Molecule type: protein

A:Residues: 279-322 <CDR>

R:Kondiah, P.; Van Obberghen-Schilling, E.; Ludwig, R.L.; Dhaf, R.; Sporn, M.B.; Rob

J. Biol. Chem. 263, 18313-18317, 1988

A:Title: CDNA cloning of porcine transforming growth factor-beta 1 mRNA. Evidence fo

A:Reference number: I46657; MUID:89054010; PMID:2461367

A:Accession: I46657

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-390 <CDR>

A:Cross-references: GB:M23703; NID:g755044; PIDN:AAA64616.1; PID:g755045

C:Genetics:

A:Gene: TGF-beta-1

C:Superfamily: Inhibin

C:Keywords: growth factor

Query Match

Best Local Similarity 94.2%; Score 2033.5; DB 2; Length 390;

Matches 387; Conservative 0; Mismatches 3; Indels 17; Gaps 1;

QY	1	MAPSGRLPLPLPLMLLVTPGRPAAGLSTCKITIDELVRRKRIRAEIRGOILSLRLA	60
DB	1	MPPSGRLPLPLPLMLLVTPGRPAAGLSTCKITIDELVRRKRIRAEIRGOILSLRLA	60
QY	61	SPPSGDVPPGPIPAVALINSTRDRAVAGEVPEPEPEADYVYKEVYRVLMVESGNOI	120
DB	61	SPPSGDVPPGPIPAVALINSTRDRAVAGEVPEPEPEADYVYKEVYRVLMVESGNOI	120
QY	121	YDKFGRGTHSLYMLFNTSELREAVEPEVYLSRAELRLRLKLKVEQHVELYQKYSNDSMR	180
DB	121	YDKFGRGTHSLYMLFNTSELREAVEPEVYLSRAELRLRLKLKVEQHVELYQKYSNDSMR	180
QY	181	YLSNRLAPSDSPFWLSFDVTVGVVROWILTRREALGFRLSAHSSSSDSKNTLHVEINGEN	240

A:Title: Nucleotide sequence of CHICKEN transforming growth factor-beta 1 (TGF-beta 1)
A:Reference number: 501413, MUID:88335639, PMID:1316520
A:Accession number: 501413
A:Molecule type: DNA
A:Residues: 1-391 <DUAK>
A:Cross-references: EMBL:X12373, NID:G63808, PIDN:CAA30933.1, PID:G63809
C:Superfamily: Inhibin
C:Keywords: growth factor

```
transforming growth factor beta-1 - sheep (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries
C.Date: 19-Dec-1997 #sequence_revision 19-Dec-1997
C.Accession: I46463, S45115 #text_change 24-Nov-1999
R.Woodall, C.J.; McLaren, L.J.; Watt, N.J.
```

Query Match	89.4%;	Score 1929.5;	DB 2;	Length 390;
Best Local Similarity	89.7%;	Pred. No. 1.5e-147;		
Matches 365;	Conservative 10;	Mismatches 15;	Indels 17;	Gaps 1

RESULT 4
WFHU2

transforming growth factor beta-1 precursor [validated] - human
N:Alternate names: growth-inhibitory factor; TGF type 2; TGF-beta
C:Species: Homo sapiens (man)
C>Date: 28-Feb-1986 #sequence_revision 19-Oct-1995 #text_change 08-Dec-2000
C:Accession: A27513; A01395; A22290; I59664; S53444
R:Bernyck, R.; Rhee, L.; Chen, E.Y.; Van Tilburg, A.
Nucleic Acids Res. 15, 3188-3189, 1987
A:Title: Intron-exon structure of the human transforming growth factor-beta precursor
A:Reference number: A27513; MUID:87174845; PMID:3470709
A:Accession: A27513
A:Molecule type: DNA
A:Residues: 1-390 <DE>
A:Cross-references: GB:X05839; GB:Y00112; NID:937097; PIDN:CAA29283.1; PID:91212989
R:Bernyck, R.; Jarrett, J.A.; Chen, E.Y.; Eaton, D.H.; Bell, J.R.; Assolian, R.K.; Rob
Nature 316, 701-705, 1985
A:Title: Human transforming growth factor-beta complementary DNA sequence and express
A:Reference number: A01395; MUID:85296301; PMID:3861940
A:Accession: A01395
A:Molecule type: mRNA
A:Residues: 1-9, 'P', 11-24, 'P', 26-159, 'R', 160-390 <DE>
A:Cross-references: GB:X02812; GB:J05114; NID:937092; PIDN:CAA26580.1; PID:937093
A:Note: the authors suggest that residues 8-23 could represent the hydrophobic core o
R:Massague, J.; Like, B.
J. Biol. Chem. 260, 2636-2645, 1985
A:Title: Cellular receptors for type beta transforming growth factor. Ligand binding
A:Reference number: A22290; MUID:85131019; PMID:2982829
A:Accession: A22290

A:Molecule type: protein
 A:Residues: 279-295,'XX',298-301 <MAS>
 A:Rutshizaki, Y.; Nitsui, Y.; Terui, T.; Koshida, Y.; Mahara, K.; Kohgo, Y.; Urushizaki, Tumor Res. 22, 41-55, 1987
 A:Title: Cloning and expression of the gene for human transforming growth factor-beta 1
 A:Reference number: 159664
 A:Accession: 159664
 A:Molecule type: mRNA
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 279-390 <RSS>
 A:Cross-references: GB:M38449; NID:9339557; PIDN:AAA36735.1; PID:9339558
 A:Stam, K.; Stewart, A.A.; Qu, G.Y.; Iwata, K.K.; Fenyoe, D.; Chait, B.T.; Marshak, D.R. Biochem. J. 305, 87-92, 1995
 A:Title: Physical and biological characterization of a growth-inhibitory activity purified from human placenta
 A:Reference number: S53444; MUID:95126934; PMID:7826358
 A:Accession: S53444
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 279-297 <STA>
 A:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide C:Genetics:
 A:Gene: GDB:TCF81; TGF β
 A:Cross-references: GDB:120729; OMIM:190180
 A:Map position: 19q13.2-19q13.2
 C:Superfamily: Inhibin
 C:Keywords: glycoprotein; growth factor; homodimer; mitogen; transformation
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-278/Domain: propeptide #status predicted <PRO>
 F:244-246/Region: cell attachment (R-G-D) motif
 F:279-390/Product: transforming growth factor beta-1 #status experimental <MAT>
 F:92,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.8%; Score 1916.5; DB 1; Length 390;
 Best Local Similarity 89.7%; Pred. No. 1.7e-146;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRRIEATRGQILSKRLA 60
 DB 1 MPSPGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRRIEATRGQILSKRLA 60
 QY 61 SPSPGDPVPGPLPEAVLALYNSTRDRAVAGESEPEPEADYAKETRVLMVETGNEI 120
 DB 61 SPSPGDPVPGPLPEAVLALYNSTRDRAVAGESEPEPEADYAKETRVLMVETGNEI 120
 QY 121 YDKKGTGPHSLYMLFNTSELREAVPEPVLLSRALRLRLKLEQVHVELYOKYSNDSMR 180
 DB 121 YDKKGTGPHSLYMLFNTSELREAVPEPVLLSRALRLRLKLEQVHVELYOKYSNDSMR 180
 QY 181 YCFSTKRNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIMSLDQYSKVLALY 240
 DB 181 YCFSTKRNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIMSLDQYSKVLALY 240
 QY 241 SGRGDLATIHGMNRPFLMATPLERAQHLSSRRRALDNTSYRYDVYASIALDTN 300
 DB 241 SGRGDLATIHGMNRPFLMATPLERAQHLSSRRRALDNTSYRYDVYASIALDTN 300
 QY 301 YCFSTKRNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIMSLDQYSKVLALY 360
 DB 301 YCFSTKRNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIMSLDQYSKVLALY 360
 QY 361 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKS 407
 DB 361 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKS 407
 QY 344 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKS 390
 DB 344 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKS 390

RESULT 5
 A6960
 transforming growth factor beta-1 precursor - green monkey
 C:Species: Cercopithecus aethiops (green monkey, grivet)
 C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 24-Nov-1999
 C:Accession: A26960
 R:Shaples, K.; Ploewman, G.D.; Rose, T.M.; Twardzik, D.R.; Purchio, A.F.
 DNA 6, 239-244, 1987

A:Title: Cloning and sequence analysis of simian transforming growth factor-beta cDNA
 A:Reference number: A26960; MUID:87246074; PMID:3474130
 A:Accession: A26960
 A:Molecule type: mRNA
 A:Residues: 1-390 <SHA>
 A:Cross-references: GB:M16658; NID:9176552; PIDN:AAA35369.1; PID:9176553
 C:Superfamily: Inhibin
 C:Keywords: growth factor
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-390/Product: transforming growth factor beta #status predicted <MAT>
 F:17-390/Product: transforming growth factor beta 1 #status predicted <MAT>

Query Match 88.7%; Score 1914.5; DB 2; Length 390;
 Best Local Similarity 89.4%; Pred. No. 2.4e-146;
 Matches 364; Conservative 10; Mismatches 16; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRRIEATRGQILSKRLA 60
 DB 1 MPSPGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRRIEATRGQILSKRLA 60
 QY 61 SPSPGDPVPGPLPEAVLALYNSTRDRAVAGESEPEPEADYAKETRVLMVETGNEI 120
 DB 61 SPSPGDPVPGPLPEAVLALYNSTRDRAVAGESEPEPEADYAKETRVLMVETGNEI 120
 QY 121 YDKKGTGPHSLYMLFNTSELREAVPEPVLLSRALRLRLKLEQVHVELYOKYSNDSMR 180
 DB 121 YDKKGTGPHSLYMLFNTSELREAVPEPVLLSRALRLRLKLEQVHVELYOKYSNDSMR 180
 QY 181 YCFSTKRNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIMSLDQYSKVLALY 240
 DB 181 YCFSTKRNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIMSLDQYSKVLALY 240
 QY 241 SGRGDLATIHGMNRPFLMATPLERAQHLSSRRRALDNTSYRYDVYASIALDTN 300
 DB 241 SGRGDLATIHGMNRPFLMATPLERAQHLSSRRRALDNTSYRYDVYASIALDTN 300
 QY 301 YCFSTKRNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIMSLDQYSKVLALY 360
 DB 301 YCFSTKRNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIMSLDQYSKVLALY 360
 QY 361 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKS 407
 DB 361 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKS 407
 QY 344 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKS 390
 DB 344 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKS 390

RESULT 6
 JC4023
 transforming growth factor beta-1 - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 24-Nov-1999
 C:Accession: JC4023
 R:Manning, A.M.; Auchampach, J.A.; Drong, R.F.; Slightom, J.L.
 Gene 155, 307-308, 1995
 A:Title: Cloning of a canine cDNA homologous to the human transforming growth factor- β
 A:Reference number: JC4023; MUID:95237630; PMID:7721110
 A:Accession: JC4023
 A:Molecule type: mRNA
 A:Residues: 1-390 <MAN>
 A:Cross-references: GB:I34936; NID:9516071; PIDN:AAA51458.1; PID:9516072
 C:Comment: This factor plays a multifunctional role as a regulator of mammalian cell C:Genetics:
 A:Gene: tgf- β 1
 C:Superfamily: Inhibin
 C:Keywords: growth factor; transforming protein
 F:1-390/Product: transforming growth factor beta 1 #status predicted <MAT>
 F:288-390/Product: transforming growth factor beta 1 #status predicted <MAT>

Query Match 87.7%; Score 1893.5; DB 2; Length 390;
 Best Local Similarity 88.7%; Pred. No. 1.2e-144;
 Matches 361; Conservative 12; Mismatches 17; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRRIEATRGQILSKRLA 60
 DB 1 MPSPGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRRIEATRGQILSKRLA 60

DB 284 YGSSSTENKNCVROLIYDERKDLGMKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLAALY 343

QY 361 NQHNRPASAPCCVPQALPEPLIYVYVGRKPKVEQLSNMIVRSCKCS 407

DB 344 NQHNRPASAPCCVPQALPEPLIYVYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 9

A40057

transforming growth factor beta-1 precursor - bovine (fragment)

N:Alternate names: beta-TGF; cartilage-inducing factor-A; EGF-dependent TGF or deGF; MGF

C:Species: Bos primigenius taurus (cattle)

C:Date: 28-Feb-1992 #sequence-revision 28-Feb-1992 #text-change 16-Jul-1999

C:Accession: A40057; A42320; A05284; A24322; B61439

R:Van Obberghen-Schilling, E.; Kondratiah, P.; Ludwig, R.L.; Sporn, M.B.; Baker, C.C.

Mol. Endocrinol. 1, 693-698, 1987

A:Title: Complementary deoxyribonucleic acid cloning of bovine transforming growth facto

A:Reference number: A40057; MUID:91042552; PMID:3153459

A:Accession: A40057

A:Molecule type: mRNA

A:Residues: 1-315 <VAN>

A:Cross-references: GB:M36271; NID:g163747; PIDN:AAA30778.1; PID:g163748

R:Ogawa, Y.; Schmidt, D.K.; Dasch, J.R.; Chang, R.J.; Glaser, C.B.

J. Biol. Chem. 267, 2325-2328, 1992

A:Title: Purification and characterization of transforming growth factor-beta2.3 and -be

A:Reference number: A42320; MUID:92129307; PMID:1733936

A:Accession: A42320

A:Molecule type: protein

A:Residues: 204-209, 'X', 211-217 <OGA>

R:Roberts, A.B.; Anzano, M.A.; Meyers, C.A.; Wideman, J.; Blacher, R.; Pan, Y.C.E.; Stei

Biochemistry 22, 5692-5698, 1993

A:Title: Purification and properties of a type beta transforming growth factor from bovi

A:Reference number: A05284; MUID:84104793; PMID:6607069

A:Accession: A05284

A:Molecule type: protein

A:Residues: 204-218 <ROB>

R:Sejedin, S.M.; Thompson, A.Y.; Bentz, H.; Rosen, D.M.; McPherson, J.M.; Conti, A.; Sig

J. Biol. Chem. 261, 5693-5695, 1986

A:Title: Cartilage-inducing factor-A. Apparent identity to transforming growth factor-be

A:Reference number: A24322; MUID:86195954; PMID:3754555

A:Accession: A24322

A:Molecule type: protein

A:Residues: 204-233 <SEY>

R:Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.

J. Protein Chem. 10, 565-575, 1991

A:Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta

A:Reference number: A61439; MUID:92189724; PMID:1799413

A:Accession: B61439

A:Molecule type: protein

A:Residues: 204-209, 'X', 211-217, 'XX', 220-232 <JIN>

C:Comment: This polypeptide is composed of two polypeptide chains cross-linked by disulf

C:Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic mitogenic a

C:Superfamily: Inhibin

C:Keywords: glycoprotein; growth factor; heterodimer

F:204-315/Product: transforming growth factor beta-1 #status experimental <MAT>

F:7,61,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.8%; Score 1572.5; DB 2; Length 315;

Best Local Similarity 88.9%; Pred. No. 6.1e-119;

Matches 295; Conservative 9; Mismatches 11; Indels 17; Gaps 1;

DB 76 AVIALKNSRDRAGSVEPEPEADYAKETRYVLMVESGNOIYDKFGKTPHSLYMLF 135

1 AIIALNSTRDRAGSAGETPEPEADYAKETRYVLMVESGKNIYDKMSSSHSIYMF 60

QY 136 NITSELREAVEPEVLLSRALRLRLKLVQHVLLYOKYSNDSRRYISNRLIASDSPEW 195

DB 61 NITSELREAVEPEVLLSRADYRLRLKLVQHVLLYOKYSNDSRRYISNRLIASDSPEW 120

QY 196 LSPDYGVVQWILTRRAIGFRLSAHSSSDSKDNTLHVEINGNSGRGLATIHGMNR 255

DB 121 LSPDYGVVQWILTRREIEGRFLSAHSCSDSKDNTLOVDINGSSGRGLATIHGMNR 180

QY 256 PELLMATPLERAQHHSRRHRRALDTNSYPYDVPYASLALDTNYCESSTENKNCVROL 315

DB 181 PELLMATPLERAQHHSRRHRRALDTNSYPYDVPYASLALDTNYCESSTENKNCVROL 223

QY 316 YIDFRKDLGMKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLAALYQHNPGASAPCCVP 375

DB 224 YIDFRKDLGMKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLAALYQHNPGASAPCCVP 283

QY 376 QALEPLIYVYVGRKPKVEQLSNMIVRSCKCS 407

DB 284 QALEPLIYVYVGRKPKVEQLSNMIVRSCKCS 315

RESULT 10

A41918

transforming growth factor beta-4 precursor - chicken (fragment)

N:Alternate names: TGF-beta 4

C:Species: Gallus gallus (chicken)

C:Date: 31-Dec-1993 #sequence-revision 31-Dec-1993 #text-change 16-Jul-1999

C:Accession: A41918; A34941; S03110

R:Butt, D.W.; Jakowlew, S.B.

Mol. Endocrinol. 6, 989-992, 1992

A:Title: Correction: a new interpretation of a chicken transforming growth factor-bet

A:Reference number: A41918; MUID:92357039; PMID:1353860

A:Accession: A41918

A:Molecule type: mRNA

A:Residues: 1-373 <BUR>

A:Cross-references: GB:M31160; GB:X08012; GB:S41706; NID:g1262437; PIDN:AB05637.1; P

A:Note: Sequence extracted from NCBI backbone (NCBI:110186, NCBI:110187)

R:Jakowlew, S.B.; Dillard, P.D.; Sporn, M.B.; Roberts, A.B.

Mol. Endocrinol. 2, 1186-1195, 1988

A:Title: Complementary deoxyribonucleic acid cloning of a messenger ribonucleic acid

A:Reference number: A34941; MUID:89112198; PMID:2464131

A:Accession: A34941

A:Molecule type: mRNA

A:Residues: 1-MDPSIGSCGSGSEFWPPGTAWSIGSRATASSCGTSKRYRAVGRAL, 122-209, 'D', 211-37

A:Cross-references: EMBL:X08012

C:Superfamily: Inhibin

C:Keywords: glycoprotein; growth factor

F:1/Domain: signal sequence (fragment) #status predicted <SIG>

F:223-225/Region: cell attachment (R-G-D) motif

F:260-373/Product: transforming growth factor beta-4 #status predicted <MAT>

F:54,109,153/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 48.5%; Score 1047; DB 2; Length 373;

Best Local Similarity 52.9%; Pred. No. 1.6e-76;

Matches 207; Conservative 52; Mismatches 100; Indels 32; Gaps 8;

DB 30 LSTCKTIMELVKKRRIRAIRGQILSKRLASPPSGDVPFGPLPAVALYNSTRDRA 89

2 LSTCKRLDEAKKKRIEAVRQILSKRLTAPPASETPPRLPDVALNSTQELK 61

QY 90 GES-VEPEPEADYAKETRYVLMVESGNOIYDKFGKTPHSLYMLFSEAVEPEV 148

DB 62 QRARLRPPDGDVEYAKELRIPIETTWGCAEMHQPOSHSTFFPNVSRARRG-GRPT 120

QY 149 LLSRAELRLRLKLVQHVLLYOKYSNDSRRYISNRLIASDSPEWLSFDVTGV 203

DB 121 LLSRAELRLRLKLVQHVLLYOKYSNDSRRYISNRLIASDSPEWLSFDVTGV 180

QY 204 VROMLTRRAIEGFRLSAHSDD---SKDNTLHVEINGNSGRGLATIHGMNR--PFL 258

DB 181 VROMLTRRAIEGFRLSAHSDD---SKDNTLHVEINGNSGRGLATIHGMNR--PFL 239

QY 259 LLMAPPLERAQHLHSRRHRRALDTNSYPYDVPYASLALDTNYCF--SSTENKNCVROL 316

DB 240 LLMAPPLERAQHLHSRRHRRALDTNSYPYDVPYASLALDTNYCF--SSTENKNCVROL 282

QY 317 IDFRKDLGMKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLAALYQHNPGASAPCCVPQ 376


```

Db 227 IEGF-PALRGDGLASLSKENTKPYLMTSMAPERIDVTSSRKKR----- 270
Oy 294 SLALDNTNCCSSTKKNCCVRLYIDFRKDLGKWIHEBKGYHANFCGPGYISLDTQY 353
    :      :      :      :      :      :      :      :      :      :
Db 271 --GVGEYECGNGNPGNCVRLYINFRKDLGKWIHEBKGYEANYCIGNCPYISMDOY 328
Oy 354 SKYLAALYNQHNPGASAPCCVPALEPLPIYTYGGRKKPVQOLSMTYRSKCS 407
    :      :      :      :      :      :      :      :      :      :
Db 329 SKYLSALYNQHNPGASAPCCVPALEPLPIYTYGGRKKPVQOLSMTYRSKCS 382

RESULT 13
Transforming growth factor beta-3 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C:Accession: S01825
R:Derynck, R.; Landquist, P.B.; Lee, A.; Wen, D.; Tamm, J.; Graycar, J.L.; Mas
EMBO J 7, 3737-3743, 1988
A:Title: A new type of transforming growth factor-beta, TGF-beta3.
A:Reference number: S01824; MUID:89031120; PMID:3208746
A:Accession: S01825
A:Molecule type: mRNA
A:Residues: 1-409 <DER>
A:Cross-references: EMBL:X14150; NID:92127; PIDN:CAA32363.1; PID:92128
C:Superfamily: Inhibin
C:Keywords: growth factor
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-297/Domain: propeptide #status predicted <PRO>
F:298-409/Product: transforming growth factor beta-3 #status predicted <MAT>

Query Match      38.6%; Score 834; DB 2; Length 409;
Best Local Similarity 44.6%; Pred. No. 2.6e-59;
Matches 190; Conservative 58; Mismatches 122; Indels 56; Gaps 14;

Oy 15 LMLLVLPGRPAAGLSTCKTIDMELVKKRIEALRGQILSKRLASPPSGDVPKPLP 74
    :      :      :      :      :      :      :      :      :      :
Db 7  LVALLNLNFAIVSLMSCTCTLDPDHKKRVEALRGQILSKRLASPPSPML--ANIP 64
    :      :      :      :      :      :      :      :      :      :
Oy 75 EAVLALYNSTR---DRVAGSEV--PEPEPADYAKETRYLVM---ESGNOIYDKFKG 126
    :      :      :      :      :      :      :      :      :      :
Db 65 YQVLDLYNSTRELLEVHGERDCTQENTSESYAKELFKDMIOGLEHNDLAVCPKG 124
    :      :      :      :      :      :      :      :      :      :
Oy 127 TPHSLYMFLNFTSELREAVPEVLLSRALRLRL---KLKVEQHVELYQKYSND----S 178
    :      :      :      :      :      :      :      :      :      :
Db 125 ITSKEFR-FNVSSVSK---NETNLFRAEFRVLRMPSSKRSQRLELQILDPDEHIAK 180
    :      :      :      :      :      :      :      :      :      :
Oy 179 WRYSLNRLAPSDSPFWLSFDVTGYVROWLTRREALIEGRLSAH-----SSDSKDN- 230
    :      :      :      :      :      :      :      :      :      :
Db 181 QRYIGKMLPFRGAEMWLSFDVTGYREWLRLRESNLGLEISIHCPCHTFQPGDILLENI 240
    :      :      :      :      :      :      :      :      :      :
Oy 231 --TLHVEINGNS---GRRGLATIGHM--NRPELLMATPLERAQH--LHSSRRRALD 281
    :      :      :      :      :      :      :      :      :      :
Db 241 QEVMIEIKRGVSEDDPGDGLGRLLKKKEHSHLLTLMMPRLDPLGLGAQRKKR--- 297
    :      :      :      :      :      :      :      :      :      :
Oy 282 TNSYRVDVPAASLADNTNCCSSTKKNCCVRLYIDFRKDLGKWIHEBKGYHANFCG 341
    :      :      :      :      :      :      :      :      :      :
Db 288 -----ALDTNYCFRNLEENCCVRLYIDFRQDLGKWIHEBKGYAANCSCG 343
    :      :      :      :      :      :      :      :      :      :
Oy 342 PCPYIWSLDTQYSKYLAALYNQHNPGASAPCCVPALEPLPIYTYGGRKKPVQOLSMTY 401
    :      :      :      :      :      :      :      :      :      :
Db 344 PCPYIRASADTHTSSVLYGLVNTLNPEASAPCCVPALEPLPIYTYGGRKKPVQOLSMTY 403
Oy 402 RSKCS 407
    :      :      :      :      :      :      :      :      :      :
Db 404 KSKCS 409

RESULT 14
A41397
transforming growth factor beta-3 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 16-Jul-1999

```

```

C:Accession: A41397; A61039; A61225
R:Miller, D.A.; Lee, A.; Matsui, Y.; Chen, E.Y.; Moses, H.L.; Derynck, R.
Mol. Endocrinol. 3, 1926-1934, 1989
A:Title: Complementary DNA cloning of the murine transforming growth factor-beta3 (TG
t tissues.
A:Reference number: A41397; MUID:90190650; PMID:2628730
A:Accession: A41397
A:Molecule type: mRNA
A:Residues: 1-410 <MIT>
A:Cross-references: GB:M32745; NID:9201949; PIDN:AAA40422.1; PID:9201950
R:Denhez, F.; Jafariz, R.; Kondatiah, P.; Roberts, A.B.; Sporn, M.B.
A:Title: Cloning by polymerase chain reaction of a new mouse TGF-beta3.
A:Reference number: A61039; MUID:91000714; PMID:2206556
A:Accession: A61039
A:Molecule type: mRNA
A:Residues: 1-410 <DEN>
R:Watrin, F.; Scotto, L.; Assouan, R.K.; Wolgemuth, D.J.
Cell Growth Differ. 2, 77-83, 1991
A:Title: Cell lineage specificity of expression of the murine transforming growth fac
A:Reference number: A61225; MUID:91299576; PMID:2069871
A:Accession: A61225
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 285-410 <MAT>
C:Superfamily: Inhibin
C:Keywords: glycoprotein; growth factor; growth regulation
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-268/Domain: propeptide #status predicted <PRO>
F:259-261/Region: cell attachment (R-G-D) motif
F:299-410/Product: transforming growth factor beta-3 #status predicted <MAT>
F:72,133,140/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      38.3%; Score 827.5; DB 2; Length 410;
Best Local Similarity 44.2%; Pred. No. 8.6e-59;
Matches 188; Conservative 57; Mismatches 127; Indels 53; Gaps 13;

Oy 15 LMLLVLPGRPAAGLSTCKTIDMELVKKRIEALRGQILSKRLASPPSGDVPKPLP 74
    :      :      :      :      :      :      :      :      :      :
Db 7  LVALLNLNFAIVSLMSCTCTLDPDHKKRVEALRGQILSKRLASPPSPML--HNP 64
    :      :      :      :      :      :      :      :      :      :
Oy 75 EAVLALYNSTR---DRVAGSEV--PEPEPADYAKETRYLVM---ESGNOIYDKFKG 126
    :      :      :      :      :      :      :      :      :      :
Db 65 YQVLDLYNSTRELLEVHGERDCTQENTSESYAKELFKDMIOGLEHNDLAVCPKG 124
    :      :      :      :      :      :      :      :      :      :
Oy 127 TPHSLYMFLNFTSELREAVPEVLLSRALRLRL---KLKVEQHVELYQKYSND----S 178
    :      :      :      :      :      :      :      :      :      :
Db 125 ITSKEFR-FNVSSVSK---NETNLFRAEFRVLRMPSSKRSQRLELQILDPDEHIAK 180
    :      :      :      :      :      :      :      :      :      :
Oy 179 WRYSLNRLAPSDSPFWLSFDVTGYVROWLTRREALIEGRLSAH-----SSDSKDN- 230
    :      :      :      :      :      :      :      :      :      :
Db 181 QRYIGKMLPFRGAEMWLSFDVTGYREWLRLRESNLGLEISIHCPCHTFQPGDILLENI 240
    :      :      :      :      :      :      :      :      :      :
Oy 231 --TLHVEINGNS---GRRGLATIGHM--NRPELLMATPLERAQH--LHSSRRRALD 282
    :      :      :      :      :      :      :      :      :      :
Db 241 HEVMEIKRGVSEDDPGDGLGRLLKKKEHSHLLTLMMPRLDPLGLGAQRKKR--- 296
    :      :      :      :      :      :      :      :      :      :
Oy 283 TNSYRVDVPAASLADNTNCCSSTKKNCCVRLYIDFRKDLGKWIHEBKGYHANFCG 342
    :      :      :      :      :      :      :      :      :      :
Db 287 -----KRALDTNCFRNLEENCCVRLYIDFRQDLGKWIHEBKGYAANCSCG 345
    :      :      :      :      :      :      :      :      :      :
Oy 343 CPYIWSLDTQYSKYLAALYNQHNPGASAPCCVPALEPLPIYTYGGRKKPVQOLSMTY 402
    :      :      :      :      :      :      :      :      :      :
Db 346 CPYIRASADTHTSSVLYGLVNTLNPEASAPCCVPALEPLPIYTYGGRKKPVQOLSMTY 405
Oy 403 SCKCS 407
    :      :      :      :      :      :      :      :      :      :
Db 406 SKCS 410

RESULT 15
A55706
transforming growth factor beta-3 precursor - rat

```


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OW protein - protein search, using sw model

Run on: April 15, 2003, 12:00:43 ; Search time 24 Seconds
(without alignments)
498,964 Million cell updates/sec

Title: US-10-017-372E-37

Perfect score: 2159

Sequence: 1 MAPSGRLPLPLPLMLIV.....GRKPKVEQLSNMIVRSCKS 407

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1919.5	88.9	390	1 US-08-132-405-1	Sequence 1, Appl
2	1919.5	88.9	390	1 US-08-395-939A-1	Sequence 1, Appl
3	1919.5	88.9	390	5 PCT-US91-01861-1	Sequence 1, Appl
4	1919.5	88.9	390	6 5168051-2	Patent No. 5168051
5	1914.5	88.7	390	1 US-07-669-171-2	Sequence 2, Appl
6	1909	88.4	394	5 PCT-US94-03705-5	Sequence 5, Appl
7	828.5	38.4	412	1 US-08-132-405-3	Sequence 3, Appl
8	828.5	38.4	412	1 US-08-395-939A-3	Sequence 3, Appl
9	824.5	38.2	412	4 US-09-380-662-21	Sequence 21, Appl
10	824.5	38.2	412	5 PCT-US91-04541-2	Sequence 2, Appl
11	824.5	38.2	412	6 5262319-2	Patent No. 5262319
12	823.5	38.1	410	5 PCT-US91-01861-3	Sequence 3, Appl
13	809	37.5	414	1 US-08-132-405-2	Sequence 2, Appl
14	809	37.5	414	1 US-08-395-939A-2	Sequence 2, Appl
15	809	37.5	414	5 PCT-US94-03705-6	Sequence 6, Appl
16	804	37.2	414	5 PCT-US91-01861-2	Sequence 2, Appl
17	803	37.2	304	1 US-08-132-405-4	Sequence 4, Appl
18	803	37.2	304	1 US-08-395-939A-4	Sequence 4, Appl
19	803	37.2	304	5 PCT-US91-01861-4	Sequence 4, Appl
20	802	37.1	414	6 5221620-4	Patent No. 5221620
21	800.5	37.1	455	6 5221620-11	Patent No. 5221620
22	793	36.7	442	6 5221620-1	Patent No. 5221620
23	753.5	34.9	139	4 US-08-065-444A-8	Sequence 8, Appl
24	638	29.6	112	1 US-07-979-441-1	Sequence 1, Appl
25	638	29.6	112	1 US-08-197-792-36	Sequence 36, Appl
26	638	29.6	112	1 US-08-486-057B-41	Sequence 41, Appl
27	638	29.6	112	1 US-08-459-850-36	Sequence 36, Appl

28	638	29.6	112	1 US-08-459-214-36	Sequence 36, Appl
29	638	29.6	112	1 US-08-470-837-30	Sequence 30, Appl
30	638	29.6	112	2 US-08-789-588-41	Sequence 41, Appl
31	638	29.6	112	2 US-08-410-573-1	Sequence 1, Appl
32	638	29.6	112	3 US-09-123-233-2	Sequence 2, Appl
33	638	29.6	112	3 US-08-927-433-5	Sequence 5, Appl
34	638	29.6	112	4 PCT-US93-03068-1	Sequence 30, Appl
35	638	29.6	112	5 PCT-US93-03068-1	Sequence 1, Appl
36	638	29.6	114	2 US-08-481-377-23	Sequence 23, Appl
37	638	29.6	114	2 US-08-491-835-21	Sequence 21, Appl
38	638	29.6	114	3 US-09-153-733A-23	Sequence 23, Appl
39	638	29.6	114	3 US-08-946-092A-21	Sequence 21, Appl
40	638	29.6	114	4 US-09-172-062-21	Sequence 21, Appl
41	638	29.6	114	4 US-08-624-635-22	Sequence 22, Appl
42	638	29.6	114	4 US-09-301-520D-21	Sequence 21, Appl
43	638	29.6	114	4 US-09-389-705-23	Sequence 23, Appl
44	638	29.6	114	5 PCT-US94-00666-23	Sequence 23, Appl
45	638	29.6	114	5 PCT-US94-00665-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-132-405-1
; Sequence 1, Application US/08132405
; Patent No. 5409896
; GENERAL INFORMATION:
; APPLICANT: Ammann, Arthur J.
; APPLICANT: Rudman, Christopher G.
; TITLE OF INVENTION: Method of Inducing Bone Growth Using
; TITLE OF INVENTION: TGF-Beta
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/132,405
; FILING DATE: 06-OCT-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/063841
; FILING DATE: 18-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/790856
; FILING DATE: 12-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/401906
; FILING DATE: 01-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 597D1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-132-405-1

Query Match 88.9%; Score 1919.5; DB 1; Length 390;
 Best Local Similarity 89.7%; Pred. No. 3e-169;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKRKRIEAIKQILSKRLA 60
 1 MPPSGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKRKRIEAIKQILSKRLA 60
 61 SPPSGDVPDPGLPEAVLALYNSTRDRAVAGESVPEPEPEADYAKETRYLVWESGNOI 120
 61 SPPSGDVPDPGLPEAVLALYNSTRDRAVAGESVPEPEPEADYAKETRYLVWESGNOI 120
 61 SPPSGDVPDPGLPEAVLALYNSTRDRAVAGESVPEPEPEADYAKETRYLVWESGNOI 120
 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLRLKLYEQHVELYKXYSNDSWR 180
 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLRLKLYEQHVELYKXYSNDSWR 180
 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLRLKLYEQHVELYKXYSNDSWR 180
 181 YLSNRLAASDSPEWLSFDYGVVROWLSTRGELIEGFRLSAHCSDSRDNTLOVDINGFT 240
 181 YLSNRLAASDSPEWLSFDYGVVROWLSTRGELIEGFRLSAHCSDSRDNTLOVDINGFT 240
 241 SGRRGDLATIGHMNRPFLLMATPLERAQHLSSRRRLALDTNSYPDYVASYALADTN 300
 241 SGRRGDLATIGHMNRPFLLMATPLERAQHLSSRRRLALDTNSYPDYVASYALADTN 300
 301 YCFSSTEKNCVQOLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTQYSKVALY 360
 284 YCFSSTEKNCVQOLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTQYSKVALY 343
 361 NQHNPGASAPCCVQALPELPYIYVYGRKPKVBOLSNMIVRSCKS 407
 344 NQHNPGASAPCCVQALPELPYIYVYGRKPKVBOLSNMIVRSCKS 390

RESULT 2
 US-08-395-939A-1
 Sequence 1, Application US/08395939A
 Patent No. 5604204
 GENERAL INFORMATION:
 APPLICANT: Ammann, Arthur J.
 APPLICANT: Rudman, Christopher G.
 TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING BONE
 TITLE OF INVENTION: GROWTH
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/395,939A
 FILING DATE: 27-FEB-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/132405
 FILING DATE: 12-NOV-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/063841
 FILING DATE: 18-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/790856
 FILING DATE: 12-NOV-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/401906
 FILING DATE: 1-SEP-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E.

REGISTRATION NUMBER: 28,616
 REFERENCE/DOCKET NUMBER: P0597D1C2D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1896
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 390 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-395-939A-1

Query Match 88.9%; Score 1919.5; DB 1; Length 390;
 Best Local Similarity 89.7%; Pred. No. 3e-169;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKRKRIEAIKQILSKRLA 60
 1 MPPSGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKRKRIEAIKQILSKRLA 60
 61 SPPSGDVPDPGLPEAVLALYNSTRDRAVAGESVPEPEPEADYAKETRYLVWESGNOI 120
 61 SPPSGDVPDPGLPEAVLALYNSTRDRAVAGESVPEPEPEADYAKETRYLVWESGNOI 120
 61 SPPSGDVPDPGLPEAVLALYNSTRDRAVAGESVPEPEPEADYAKETRYLVWESGNOI 120
 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLRLKLYEQHVELYKXYSNDSWR 180
 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLRLKLYEQHVELYKXYSNDSWR 180
 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLRLKLYEQHVELYKXYSNDSWR 180
 181 YLSNRLAASDSPEWLSFDYGVVROWLSTRGELIEGFRLSAHCSDSRDNTLOVDINGFT 240
 181 YLSNRLAASDSPEWLSFDYGVVROWLSTRGELIEGFRLSAHCSDSRDNTLOVDINGFT 240
 241 SGRRGDLATIGHMNRPFLLMATPLERAQHLSSRRRLALDTNSYPDYVASYALADTN 300
 241 SGRRGDLATIGHMNRPFLLMATPLERAQHLSSRRRLALDTNSYPDYVASYALADTN 300
 301 YCFSSTEKNCVQOLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTQYSKVALY 360
 284 YCFSSTEKNCVQOLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTQYSKVALY 343
 361 NQHNPGASAPCCVQALPELPYIYVYGRKPKVBOLSNMIVRSCKS 407
 344 NQHNPGASAPCCVQALPELPYIYVYGRKPKVBOLSNMIVRSCKS 390

RESULT 3
 PCT-US91-01861-1
 Sequence 1, Application PC/TUS9101861
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 TITLE OF INVENTION: Method of Pre-disposing Mammals to
 TITLE OF INVENTION: Accelerated Tissue Repair
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/01861
 FILING DATE: 19910320
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: U.S. Ser. No. 07/504,495
 FILING DATE: 4 April 1990

ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E.
 REGISTRATION NUMBER: 28, 616
 REFERENCE/DOCKET NUMBER: 637
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/266-1896
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 390 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 PCT-US91-01661-1

Query Match 88.9%; Score 1919.5; DB 5; Length 390;
 Best Local Similarity 89.7%; Pred. No. 3e-169;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 DB 1 MPSPGLRLPLPLMLVLTTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 QY 61 SPSPGQDVPPGPPEAVLALYNSTRDVAGSEVEPEPEADYAKETRVLMVESGNOI 120
 DB 61 SPSPGQDVPPGPPEAVLALYNSTRDVAGSEVEPEPEADYAKETRVLMVESGNOI 120
 QY 121 YDKFKGTPHSLYMFNTSELREAVPEVLLSRALRLRLKLKEQHELYOKYSNDSMR 180
 DB 121 YDKFKGTPHSLYMFNTSELREAVPEVLLSRALRLRLKLKEQHELYOKYSNDSMR 180
 QY 121 YDKFKGTPHSLYMFNTSELREAVPEVLLSRALRLRLKLKEQHELYOKYSNDSMR 180
 DB 121 YDKFKGTPHSLYMFNTSELREAVPEVLLSRALRLRLKLKEQHELYOKYSNDSMR 180
 QY 181 YLSNRLAPSDSPFWLSPDYTGVRQWMLSRGELIEGFRLSAHSCSDSDNTLOVDINGFT 240
 DB 181 YLSNRLAPSDSPFWLSPDYTGVRQWMLSRGELIEGFRLSAHSCSDSDNTLOVDINGFT 240
 QY 241 SGRGDLATIHGMNRPFLMLATPLERAQHLQSSRRH-----ALDTN 283
 DB 241 SGRGDLATIHGMNRPFLMLATPLERAQHLQSSRRH-----ALDTN 283
 QY 301 YCFSTKNCVCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPPIYMSLDTOYSKVALY 360
 DB 301 YCFSTKNCVCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPPIYMSLDTOYSKVALY 360
 QY 284 YCFSTKNCVCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPPIYMSLDTOYSKVALY 343
 DB 284 YCFSTKNCVCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPPIYMSLDTOYSKVALY 343
 QY 361 NOHNPASAPCCVPQALEPLTYVYVGRKPKVEOLSNMIVRSCKS 407
 DB 361 NOHNPASAPCCVPQALEPLTYVYVGRKPKVEOLSNMIVRSCKS 407
 QY 344 NOHNPASAPCCVPQALEPLTYVYVGRKPKVEOLSNMIVRSCKS 390
 DB 344 NOHNPASAPCCVPQALEPLTYVYVGRKPKVEOLSNMIVRSCKS 390

RESULT 4
 5168051-2
 Patent No. 5168051
 APPLICANT: DERVICK, RIK M. A.; GOEDEL, DAVID V.
 TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
 NUMBER OF SEQUENCES: 21
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/389, 929
 FILING DATE: 04-AUG-1989
 SEQ ID NO: 2:
 LENGTH: 390
 5168051-2

Query Match 88.9%; Score 1919.5; DB 6; Length 390;
 Best Local Similarity 89.7%; Pred. No. 3e-169;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 DB 1 MPSPGLRLPLPLMLVLTTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 QY 61 SPSPGQDVPPGPPEAVLALYNSTRDVAGSEVEPEPEADYAKETRVLMVESGNOI 120
 DB 61 SPSPGQDVPPGPPEAVLALYNSTRDVAGSEVEPEPEADYAKETRVLMVESGNOI 120

QY 121 YDKFKGTPHSLYMFNTSELREAVPEVLLSRALRLRLKLKEQHELYOKYSNDSMR 180
 DB 121 YDKFKGTPHSLYMFNTSELREAVPEVLLSRALRLRLKLKEQHELYOKYSNDSMR 180
 QY 181 YLSNRLAPSDSPFWLSPDYTGVRQWMLSRGELIEGFRLSAHSCSDSDNTLOVDINGFT 240
 DB 181 YLSNRLAPSDSPFWLSPDYTGVRQWMLSRGELIEGFRLSAHSCSDSDNTLOVDINGFT 240
 QY 241 SGRGDLATIHGMNRPFLMLATPLERAQHLQSSRRH-----ALDTN 283
 DB 241 SGRGDLATIHGMNRPFLMLATPLERAQHLQSSRRH-----ALDTN 283
 QY 301 YCFSTKNCVCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPPIYMSLDTOYSKVALY 360
 DB 301 YCFSTKNCVCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPPIYMSLDTOYSKVALY 360
 QY 284 YCFSTKNCVCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPPIYMSLDTOYSKVALY 343
 DB 284 YCFSTKNCVCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPPIYMSLDTOYSKVALY 343
 QY 361 NOHNPASAPCCVPQALEPLTYVYVGRKPKVEOLSNMIVRSCKS 407
 DB 361 NOHNPASAPCCVPQALEPLTYVYVGRKPKVEOLSNMIVRSCKS 407
 QY 344 NOHNPASAPCCVPQALEPLTYVYVGRKPKVEOLSNMIVRSCKS 390
 DB 344 NOHNPASAPCCVPQALEPLTYVYVGRKPKVEOLSNMIVRSCKS 390

RESULT 5
 US-07-669-171-2
 Sequence 2, Application US/07669171
 Patent No. 5304541
 GENERAL INFORMATION:
 APPLICANT: PURCHIO, ANTHONY F.
 APPLICANT: MADISEN, LINDA
 APPLICANT: MERWIN, JUNE RAE
 TITLE OF INVENTION: TGF-b1/b2: A NOVEL CHIMERIC TRANSFORMING
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PENNIE & EDMONDS
 STREET: 1155 AVENUE OF THE AMERICAS
 CITY: NEW YORK
 STATE: N.Y.
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/669,171
 FILING DATE: 19910314
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MISROCK, S. LESLIE
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 5624-159-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEFAX: 212-869-9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 390 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-669-171-2

Query Match 88.7%; Score 1914.5; DB 1; Length 390;
 Best Local Similarity 89.4%; Pred. No. 8.7e-169;
 Matches 364; Conservative 10; Mismatches 16; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 DB 1 MPSPGLRLPLPLMLVLTTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 QY 61 SPSPGQDVPPGPPEAVLALYNSTRDVAGSEVEPEPEADYAKETRVLMVESGNOI 120
 DB 61 SPSPGQDVPPGPPEAVLALYNSTRDVAGSEVEPEPEADYAKETRVLMVESGNOI 120

Query Match	Score 1909;	DB 5;	Length 394;
Best Local Similarity	88.48;	Pred. No. 2.8e-168;	

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896

APPLICATION NUMBER: 08/132405

; CURRENT APPLICATION NUMBER: US/05

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; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-380-662-21

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```

Query Match      38.2% Score 824.5; DB 4; Length 412;
Best Local Similarity 44.2%; Pred. No. 4.8e-68;
Matches 188; Conservative 58; Mismatches 126; Indels 53; Gaps 13;

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15 LMLVLVTPGRPAAGSTCKTIDMELVKRRRIEAIKQIISKLRLASPPSGDVPFGPLP 74
9 LVVLLALNFATVSLSTCTTLDGHIKKRKEAIKQIISKLRLTSPPEPTVMT--HVP 66
75 EAVLALYNSTR--DRVAGESE--PEPEADYAKETRVLMVE--SGNQIYDKFKG 126
67 YVVALYNSTRLEEMHREGCTQENTSEYAKETIKHFMIOGLAEHNELAVCPKG 126
127 TPHSLYMLFNTSELREAVPEPVLLSRRELRLRL--KLKVEQHVELYQKYSND----S 178
127 ITSKEVR-FNVSSVER--NRTNLFRAEFRLVLPNPSSKRNEQRIELFQILRPDEHIAK 182
179 WRYLSNRLAPSDSPMELSFDTGYVROWLTLRREALIGFRLSAH-----SSSDSKDN- 230
183 QRYIGGKNLPRTGTAEMLSFDVTDTVREMLLRRESNGLSTHCPCHTQPNQDILENT 242
231 --TLHVEINGFNS--GRGDLATIHGM--NRPELLMATPRLERAQHLSSRHRLALDT 282
243 HEVMEIKFKGVNEDDHGDLGRLLKKOKDHNPHILMMIIPRRLDNPQGGGGRK---- 298
283 NSPYDVPDYASLADTNYCFSSSTEKNCCVROLYIDFRKDLGKWHIERPGYANFCLGP 342
299 -----KRALDTNYCFRLNECCVRLYIDFRDLGKWHIEPKGYANFCSGP 347
343 CPYIWSLDTQYSKVLATYNOHNPAGASAPCCVPOALEPPIYVYGGKPKVQDLSMAYR 402
348 CPYLSADTHTSTYVGLYNTLNPEASASPCVQDLEPLTILYVGRTPKVEQLSNMVK 407
403 SCKCS 407
408 SCKCS 412

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RESULT 10
PCT-US91-04541-2
; Sequence 2, Application PC/TUS9104541
; GENERAL INFORMATION:
; APPLICANT: Oncogene Science Inc.
; TITLE OF INVENTION: TISSUE DERIVED TUMOR GROWTH INHIBITORS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/04541
; FILING DATE: 19910625
; CLASSIFICATION:

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1919/22669-F-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEEX: 422523 COOP UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-04541-2

```

```

Query Match      38.2% Score 824.5; DB 5; Length 412;
Best Local Similarity 44.2%; Pred. No. 4.8e-68;
Matches 188; Conservative 58; Mismatches 126; Indels 53; Gaps 13;

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15 LMLVLVTPGRPAAGSTCKTIDMELVKRRRIEAIKQIISKLRLASPPSGDVPFGPLP 74
9 LVVLLALNFATVSLSTCTTLDGHIKKRKEAIKQIISKLRLTSPPEPTVMT--HVP 66
75 EAVLALYNSTR--DRVAGESE--PEPEADYAKETRVLMVE--SGNQIYDKFKG 126
67 YVVALYNSTRLEEMHREGCTQENTSEYAKETIKHFMIOGLAEHNELAVCPKG 126
127 TPHSLYMLFNTSELREAVPEPVLLSRRELRLRL--KLKVEQHVELYQKYSND----S 178
127 ITSKEVR-FNVSSVER--NRTNLFRAEFRLVLPNPSSKRNEQRIELFQILRPDEHIAK 182
179 WRYLSNRLAPSDSPMELSFDTGYVROWLTLRREALIGFRLSAH-----SSSDSKDN- 230
183 QRYIGGKNLPRTGTAEMLSFDVTDTVREMLLRRESNGLSTHCPCHTQPNQDILENT 242
231 --TLHVEINGFNS--GRGDLATIHGM--NRPELLMATPRLERAQHLSSRHRLALDT 282
243 HEVMEIKFKGVNEDDHGDLGRLLKKOKDHNPHILMMIIPRRLDNPQGGGGRK---- 298
283 NSPYDVPDYASLADTNYCFSSSTEKNCCVROLYIDFRKDLGKWHIERPGYANFCLGP 342
299 -----KRALDTNYCFRLNECCVRLYIDFRDLGKWHIEPKGYANFCSGP 347
343 CPYIWSLDTQYSKVLATYNOHNPAGASAPCCVPOALEPPIYVYGGKPKVQDLSMAYR 402
348 CPYLSADTHTSTYVGLYNTLNPEASASPCVQDLEPLTILYVGRTPKVEQLSNMVK 407
403 SCKCS 407
408 SCKCS 412

```

```

RESULT 11
5262319-2
; Patent No. 5262319
; APPLICANT: IWATA, KENNETH K.; FOULKES, J. GORDON; DIJKE,
; PETER T.; HALEY, JOHN D.
; TITLE OF INVENTION: METHOD FOR OBTAINING BONE MARROW FREE
; OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/543,341
; FILING DATE: 25-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 353,410
; FILING DATE: 17-MAY-1989
; APPLICATION NUMBER: 183,410
; FILING DATE: 20-APR-1988
; APPLICATION NUMBER: 111,022
; FILING DATE: 20-OCT-1987
; APPLICATION NUMBER: 922,121
; FILING DATE: 20-OCT-1986

```



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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/132,405
FILING DATE: 06-OCT-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/063841
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790856
FILING DATE: 12-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/401906
FILING DATE: 01-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 597D1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-132,405-2

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Query Match 37.5%; Score 809; DB 1; Length 414;
Best Local Similarity 43.2%; Pred. No. 1.3e-66;
Matches 181; Conservative 62; Mismatches 116; Indels 60; Gaps 14

[illegible]

RESULT 14
 US-08-395-939A-2
 Sequence 2, Application US/08395939A
 Patent No. 5604204
 GENERAL INFORMATION:
 APPLICANT: Ammann, Arthur J.
 APPLICANT: Rudman, Christopher G.
 TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING BONE
 TITLE OF INVENTION: GROWTH
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.

```

1 STREET: 460 Point San Bruno Blvd
2 CITY: South San Francisco
3 STATE: California
4 COUNTRY: USA
5 ZIP: 94080
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: 5,25 inch, 360 Kb floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: patin (Genentech)
12
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/395,939A
15 FILING DATE: 27-FEB-1995
16 CLASSIFICATION: 514
17
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: 08/132405
20 FILING DATE: 12-NOV-1993
21
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 08/063841
24 FILING DATE: 18-MAY-1993
25
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 07/790856
28 FILING DATE: 12-NOV-1991
29
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: 07/401906
32 FILING DATE: 1-SEP-1989
33
34 ATTORNEY/AGENT INFORMATION:
35 NAME: Hasak, Janet E.
36 REGISTRATION NUMBER: 28,616
37 REFERENCE/DOCKET NUMBER: P0597D1C2D1
38
39 TELECOMMUNICATION INFORMATION:
40 TELEPHONE: 415/225-1896
41 TELEFAX: 415/952-9881
42
43 TELEX: 910/371-7168
44
45 INFORMATION FOR SEQ ID NO: 2:
46
47 SEQUENCE CHARACTERISTICS:
48 LENGTH: 414 amino acids
49 TYPE: amino acid
50 TOPOLOGY: linear
51
52 US-08-395-939A-2

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Query Match	37.5%	Score 809,	DB 1,	Length 414,
Best Local Similarity	43.2%	Pred. No. 1.3e 66,		
Matches 181; Conservative	62;	Mismatches 116;	Indels 60;	Gaps 14

QY	27	AAGSTKTIIMELVYKRRIRIAIGOLISKIRLASpEqgVp--	186	PGRLPEAVLALYNSTR	85		
		:: ::					
Dp	18	ALSTGCTSLDMQFMKRRIDAITGOLISKIRLSPbE--	191	DYPEEEVPEVISTYNSTR	75		
QY	86	D----RVAGSEVEPEE-PEADYVAKETRYLM--	137	VESGNOIDKRCRGPMSLYMLFNT	137		
		: : : : : : : :					
Dp	76	DLLOEKASRRAAACERERDEEYKAYEVKIDMPPEPSENAI	133	PPFY-RRYFRIYAFDV	133		
QY	138	SELREAVPEPILLSRAELRLRL--	186	KLK-EQVVELYQ----	KYSNDSMRYLSNRLLA	186	
		: : : : : : : :					
Dp	135	SAMEKKNASN--	191	LTKAEFRVFRLONPAPRPEQETIELYOLISKDLTSP	191	ORYIDSKVYK	191
QY	189	PSDSPEWLSEFDVYGVVQOMLTRREALIGFIRSAHSS-	235	-----	DSKDNLT	LHNE--	235
		: : : : : :					
Dp	192	TRAGEWELSPDYDAVHHEMLHKHDNRNGEFTISLHC	251	PPCTVYPSNNTIIPKNSSELEARFA	251		
QY	236	-INGFNSGRGDLATIHGMNR----	288	PELLMATPLEAHOHLHSSRRRLADTNSY	288	PYD	288
		: : : : : : : :					
Dp	252	GIDGTSTYTGSDOKTILKTRKKNSGKTPHLLMLLP	302	SRLESQQTNRKKR-----	302		
QY	289	VPDYASIALDTNNCESTENKCCVQOLYIDPFKDLGKWT	348	HERKGIYANFLCGLCPYIWS	348		
		: : : : : : :					
Dp	303	-----ALDAAACFRNVQDNCCLRPPLYIDFKRDLGKWT	355	HERKGVNANFCACAGPYLWS	355		
QY	349	LDTQYSKVIALYQNHQPGASAAAPCCVQOALEREPI	407	YVYVGRKKRQVLOLSMIVYSCKS	407		
		: : : : : : : :					
Dp	356	SPDQHRSRYLSTVNTINPEASAPCCVSOQDEPLITILY	414	IKTPTKRIQLOLSMIVYSCKS	414		

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:54:18 ; Search time 88 Seconds
(without alignments)
616.284 Million cell updates/sec

Title: US-10-017-372E-37

Sequence score: 2159
1 MAPSGIRLLPLILPLIMLV.....GRKPKVQLSNMIVRSCKCS 407

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq.101002: *
2: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT: *
3: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *
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21: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *
22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT: *
23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT: *
24: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2048.5	94.9	390	23	AAE13596 Porcine transforming
2	1926.5	89.2	390	22	AAAM39186 Human polypeptide
3	1919.5	88.9	390	7	AAPE1468 Prengf-beta gene p
4	1919.5	88.9	390	11	AAAR04034 Sequence of pre-TG
5	1919.5	88.9	390	11	AAAR05258 Human pre-transfor
6	1919.5	88.9	390	12	AAAR13813 Human pro-TGF-beta
7	1919.5	88.9	390	16	AAAR73596 Human TGF-beta 1 p
8	1919.5	88.9	390	17	AAAR90827 pre-transforming g
9	1916.5	88.8	390	23	AAU77101 Human transforming
10	1916.5	88.8	390	23	AAE16943 Human transforming

11	1914.5	88.7	390	13	AAAR20124	Sequence of simian
12	1910.5	88.5	390	15	AAAR46227	Human pre-TGF-beta
13	1909	88.4	391	16	AAAR83054	Transforming growt
14	1908.5	88.4	390	19	AAAR78785	Human pre-transfor
15	1907.5	88.4	390	22	AAAB84601	Nucleotide sequenc
16	1905	88.2	391	9	AAAR01362	Human transforming
17	1904	88.2	434	11	AAAR03743	Monkey transformin
18	1883.5	87.2	386	11	AAAR05663	Simian transformin
19	1878	87.0	387	11	AAAR05664	Simian transformin
20	1867.5	86.5	390	11	AAAR05492	Chimeric simian TG
21	1863.5	86.3	390	13	AAAR20542	TGF-beta 1/beta 2
22	1844	85.4	389	13	AAAR29657	TGF-beta 1. Homo
23	1839	85.2	453	22	AAAR40972	Human polypeptide
24	1758.5	81.4	390	13	AAAR0126	Sequence of hybrid
25	1757.5	81.4	390	11	AAAR05749	Human TGF-beta2 ex
26	1751.5	81.1	390	11	AAAR05665	Human transforming
27	1749.5	81.0	390	11	AAAR05666	Hybrid transformin
28	1742	80.7	391	10	AAAR91900	Sequence encoded b
29	1715	79.4	389	16	AAAR39921	Simian-human hybr
30	1300	60.2	278	15	AAAR53090	Simian transforming
31	1295	60.0	278	12	AAAR12541	Latency associated
32	1169	54.1	290	22	ABG06792	Novel human diagno
33	944	43.7	227	22	ABG02634	Novel human diagno
34	901	41.7	226	22	ABG02023	Novel human diagno
35	868.5	40.2	382	21	AAAB08338	Amino acid sequenc
36	868.5	40.2	382	23	AAAU77105	Novel human diagno
37	832.5	38.6	456	19	AAAR78786	Pig transforming g
38	828.5	38.4	412	16	AAAR3558	Human TGF-beta 3 p
39	826	38.3	456	15	AAAR6228	Pig TGF-beta-3. S
40	824.5	38.2	412	13	AAAR06261	Transforming Growt
41	824.5	38.2	412	19	AAAR00417	Amino acid sequenc
42	824.5	38.2	412	23	AAAU77103	Human transforming
43	824.5	38.2	412	23	ABB90765	Human Tumour Endot
44	819.5	38.0	457	11	AAAR04080	Polypeptide sequen
45	816	37.8	413	13	AAAR22038	Mutant Transformin

ALIGNMENTS

RESULT 1	AAE13596	AAE13596 standard; Protein: 390 AA.
ID	AAE13596	
AC	AAE13596	
XX	26-FEB-2002	(first entry)
DT	XX	
DE	XX	Porcine transforming growth factor beta 1 (TGF-beta1) mutant.
XX	XX	
XX	XX	Porcine; transforming growth factor beta 1; TGF-beta1; gene therapy;
KW	IBD; inflammatory bowel disease; autoimmune disease; immunosuppressive;	
KW	multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;	
KW	diabetes mellitus; sarcoidosis; psoriasis; dermatological; mutant;	
KW	mutin.	
XX	XX	
OS	Sus scrofa.	
XX	XX	
FT	Key	Location/Qualifiers
FT	Misc-difference 223	/note= "Wild type Cys substituted with Ser"
FT	Misc-difference 225	/note= "Wild type Cys substituted with Ser"
FT	FT	
XX	XX	
PN	WO200181404-A2.	
XX	01-NOV-2001.	
PD	XX	
XX	20-APR-2001; 2001WO-US12980.	
PF	XX	
XX	20-APR-2000; 2000US-199014P.	
PR	XX	
XX	XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	

XX Strober W, Nakamura K, Kitani A, Fuss IJ;
 PI WPI: 2002-026155/03.
 XX N-PSDB: AAD22696.
 DR
 XX Composition for treating autoimmune diseases e.g. inflammatory bowel
 PT disease in humans, comprises vector containing transforming growth
 XX factor-beta under the control of inducible promoter -
 XX
 XX Example 1: Fig 1: 78bp: English.

CC The invention relates to a composition containing a vector comprising a
 CC gene encoding a regulatory transcription factor under the control of a
 CC promoter encoding a transforming growth factor-beta (TGF-beta). The
 CC vector is useful for expressing TGF-beta, such as TGF-beta1, TGF-beta2
 CC or TGF-beta3, its variants or homologues, by transfecting a cell which
 CC is part of a host suspected of having an autoimmune disease, especially
 CC inflammatory bowel disease (IBD), under conditions such that the
 CC polypeptide encoded by the nucleic acid sequence in the vector is
 CC expressed. The vector is delivered using a delivery system. The delivery
 CC of the vector results in substantial elimination of symptoms of the
 CC autoimmune disease and increased production of IL-10 by the host. The
 CC composition is useful for treating various diseases with an autoimmune
 CC component such as multiple sclerosis, rheumatoid arthritis, systemic
 CC lupus erythematosus, insulin-dependent diabetes mellitus, sarcoidosis
 CC and psoriasis, and also for assaying the expression of a gene in a cell.
 CC The vector is further useful for screening of the effect of test
 CC compounds on cytokine (e.g. TGF-beta) expression of transfected cells.
 CC The present sequence is porcine TGF-beta1 mutant.

Sequence 390 AA:

Query Match 94.98; Score 2048.5; DB 23; Length 390;
 Best Local Similarity 95.88; Pred. No. 4.8e-171;
 Matches 390; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAPSGRLRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKRRRIEIRGOILSKRLA 60
 DB 1 MAPSGRLRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKRRRIEIRGOILSKRLA 60
 QY 61 SPSSQGDVPPGPPLEPAVALYNSTRDRAVAGESVEPEPEADYAKETVRVLMVESGNOI 120
 DB 61 SPSSQGDVPPGPPLEPAVALYNSTRDRAVAGESVEPEPEADYAKETVRVLMVESGNOI 120
 QY 121 YDFKCTPHSLYMLFNTSELREAVPEPVLLSRALRLRLKLKYEOHVELYOKYSNDSWR 180
 DB 121 YDFKCTPHSLYMLFNTSELREAVPEPVLLSRALRLRLKLKYEOHVELYOKYSNDSWR 180
 QY 181 YLSNRLIAPSDSEPMWLSFDYTGVRQWLTTRREALGFRLSHSSSDSKDNTLHVEINGFN 240
 DB 181 YLSNRLIAPSDSEPMWLSFDYTGVRQWLTTRREALGFRLSHSSSDSKDNTLHVEINGFN 240
 QY 241 SGRGRLATIHGNNRPFLMATPRLERAOHLHSSRRRALDNTNSYPYDVPDYLALDTN 300
 DB 241 SGRGRLATIHGNNRPFLMATPRLERAOHLHSSRRRALDNTNSYPYDVPDYLALDTN 300
 QY 301 YCFSSTKNCVAVQOLYIDPRKDLGKMKIHEPKGYHANFCIGPCQYISLDTQYSKVIALY 360
 DB 284 YCFSSTKNCVAVQOLYIDPRKDLGKMKIHEPKGYHANFCIGPCQYISLDTQYSKVIALY 360
 QY 361 NOHNPASAPCCVPOALEPLPIVYVYVGRKPKVEOLSNMIVRSCKCS 407
 DB 344 NOHNPASAPCCVPOALEPLPIVYVYVGRKPKVEOLSNMIVRSCKCS 390

RESULT 2
 AAM39186 standard: Protein; 390 AA.

XX AAM39186;
 XX 22-OCT-2001 (first entry)
 DT

XX Human polypeptide SEQ ID NO 2331.
 DE
 XX Human: nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO200153312-A1.
 PN
 XX
 XX 26-JUL-2001.
 PD
 XX
 XX 26-DEC-2000; 2000MO-US34263.
 PF
 XX
 XX 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.

(HYSF-) HYSFO INC.

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 PI
 DR WPI: 2001-442253/47.
 DR N-PSDB: AA158342.

XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 PT
 XX
 XX Example 4: SEQ ID NO 2331; 10078bp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM36642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 CC
 XX
 XX Sequence 390 AA:

Query Match 89.28; Score 1926.5; DB 22; Length 390;
 Best Local Similarity 89.98; Pred. No. 2.4e-160;
 Matches 366; Conservative 10; Mismatches 14; Indels 17; Gaps 1;

QY 1 MAPSGRLRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKRRRIEIRGOILSKRLA 60
 DB 1 MAPSGRLRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKRRRIEIRGOILSKRLA 60
 QY 61 SPSSQGDVPPGPPLEPAVALYNSTRDRAVAGESVEPEPEADYAKETVRVLMVESGNOI 120
 DB 61 SPSSQGDVPPGPPLEPAVALYNSTRDRAVAGESVEPEPEADYAKETVRVLMVESGNOI 120
 QY 121 YDFKCTPHSLYMLFNTSELREAVPEPVLLSRALRLRLKLKYEOHVELYOKYSNDSWR 180

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	52
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RESULT 3
AAP61468
ID AAP61468 standard; Protein: 390 AA.

AC AAP61468;
XX
DT 28-Oct-1991 (first entry)
XX
DE PreTGF-beta gene product.
XX
KW Transforming growth factor beta; cancer; wound healing

	Key Protein	Location/Qualifiers
FH		
FT		279..390

PN EP200341-A.

PD 10-DEC-1986.

PF 21-MAR-1986; 86EP-0302112

PR	22-MAR-1985;	85US-0715142
PR	13-MAR-1987.	87US-0025423

XX
PA (GETH) GENENTECH INC

XX Derynck RMA;
PI

AA WPI; 1986-326875/50
DR

XX

PT wounds (J6 2/9/86).

PS Disclosure; Fig 1b; 26pp; English.

The gene product is known to stimulate cell proliferation and inhibit anchorage-dependent growth of a variety of human cancer cell lines, it is esp. useful in treatment of burns and the promotion of CC surface and internal wound healing. TGF-beta may be expressed from a transformed CHO cell line.

50 Sequence 390 AA;

Query Match	88.9%	Score 1919.5	-DB 7	Length 390
Best Local Similarity	89.7%	Pred No. 9.9e-160		
Matches 365	Conservative 10	Mismatches 15	Indels 17	Gaps 1

```

Qy      1 MAPSGIRLLPLPLPLMLVLVTPGPPAGISCTCTIMELVYKRRRIEAIHQIQLSKRLA 60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MPSPGIRLLPLPLPLMLVLVTPGPPAGISCTCTIMELVYKRRRIEAIHQIQLSKRLA 60
Qy      61 SPSPGSDVPPGGLPEAVIALYNSTRDRAVAGESVEPEPEADYYAKEVTRLVAVESGNI 120

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Db	61	SPSQSGEVPPEGLPEALVALYNSTRDRVAGESAEBEPEDADYAAKEVTVLAVETHEHN	120
Qy	121	YDKFKGTPHSLYMLFNTSELREAVPEVYLSRAELRLRLKLVKEOHVELYCKYXSDSMR	180
Db	121	YDKFKQSTHSLYMFNTSELREAVPEVYLSRAELRLRLKLVKEOHVELYCKYXSNMSR	180
Qy	181	YLSRRLAPSSPEWLSFEDYTGVAWQLTGREALTEGRLSAHSSSDKNTLVEIANGFN	240
Db	181	YLSRRLAPSSPEWLSFDYTGVAWQLSRGKELEGRLSAHSCSDSRMTLOYVDINGFT	240
Qy	241	SGRRGDLATIHGMNPELLMATPRLERAÖHLSSRRRALDTNSPYDVPDYSLALDTN	300
Db	241	TGRRGDLATIHGMNPELLMATPRLERAÖHLOSSRRHR-----ALDTN	2833
Qy	301	YCESSTEKNCCVROLYIDFKRDLGWMKTHKEGVHANFCGPGCYIMSLDPTQYSKVYALY	360
Db	284	YCFSTSTEKNCCVROLYIDFKRDLGWMKTHKEGVHANFCGLPGCYIMSLDPTQYSKVYALY	343
Qy	361	NOHNPAGSAAPCCVPOALEPLIYUYUGRKPKVYOLDSNMIVSRCKS	407
Db	344	NOHNPAGSAAPCCVPOALEPLIYUYUGRKPKVYOLDSNMIVSRCKS	390

RESULT 4	
AA04034	
ID	AA04034 standard; protein; 390 AA

AC AAR04034;

DT 31-MAY-1989 (first entry)
XY

DE Sequence of pre-1GH-beta 1

KW transforming growth factor- β (TGF- β), cannot be an inhibitory.

XX	Key	Location/Qualifiers
FH		

XX
XX
XX

XX	2
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XX
XX
GENERAL ELECTRIC INC

XX
BT Deruyck PM Goeddel DV:

XX
DB WPT: 1990-007474/01.

DR N-PSDB; AAQ02013.
XX

PT probe, or to produce TGF β be

XX and no products were observed.

XX

CC 1) polypeptide and correspo

CC as a probe or to produce TG

XX
CO
Enclosure 390 AA.

Query Match: 88.98%

Best Local Similality 09.18,
Matches 365; Conservative

```

QY 1 MAPSGRLRLPLPLPLMLVLTGPRPAAGLSTCKTIDMELVKRRIRIAIRGQILSKRLA 60
D 1 MPPSGRLRLPLPLPLMLVLTGPRPAAGLSTCKTIDMELVKRRIRIAIRGQILSKRLA 60
D 61 SPPSGGVPPGRLPEAVLALYNSTRDRVAGESEVPEPEADYIAKEVTRVAVESGNOI 120
D 61 SPPSGGVPPGRLPEAVLALYNSTRDRVAGESEVPEPEADYIAKEVTRVAVESGNOI 120
QY 121 YDKFKGTPHSLVLMFNSELREAVPEPVLLSRARLRLRLKLKVEQHVLEYOKYSNDSMR 180
D 121 YDKFKQSTHSTYMFNTSELREAVPEPVLLSRARLRLRLKLKVEQHVLEYOKYSNDSMR 180
QY 181 YLSNRLAPSDSPPEWLSFDVTGVYRQMLTRRAIEGFRLSAHSSSDSKDNLTLYVEINGFN 240
D 181 YLSNRLAPSDSPPEWLSFDVTGVYRQMLTRRAIEGFRLSAHSSSDSKDNLTLYVEINGFN 240
QY 241 SGRRGDLATIHGMNRPFLLMATPLERAQHLSSRRRALDNTSPYDVPDYASLALDTN 300
D 241 TGRGDLATIHGMNRPFLLMATPLERAQHLSSRRRALDNTSPYDVPDYASLALDTN 300
QY 301 YCFSSSTEKNCCVROLYIDFRKDLGKWKIHEPKGYHANFCIGPCPYIWSLDTQYSKVLALY 360
D 284 YCFSSSTEKNCCVROLYIDFRKDLGKWKIHEPKGYHANFCIGPCPYIWSLDTQYSKVLALY 360
QY 361 NQHNPGASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 407
D 344 NQHNPGASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 5
AAR05258
AAR05258 standard; protein: 390 AA.
AAR05258:
05-AUG-1990 (first entry)
Human pre-transforming growth factor-beta-1 (pre-TGF-beta-1).
Transforming growth factor-beta-1 (TGF-beta-1);
neoplastic cell line inhibition;
EGF-potential anchorage-independent growth.
Homo sapiens.
Key Location/Qualifiers
Peptide 1..278
Protein 279..2011
Domain 8..23
Modified-site /note="hydrophobic domain"
Modified-site /note="potential N-glycosylation site"
Modified-site /note="as above"
Modified-site 176..178
Modified-site /note="as above"
Cleaveage-site 277..278
/note="proteolytic cleavage site"

US4866747-A.
12-DEC-1989.
13-MAR-1987; 87US-0025423.
13-MAR-1987; 87US-0025423, US-715142.
(GETH ) GENENTECH INC.
DeGynck RMA, Goeddel DV.
WPI: 1990-051338/07.
N-PSDB: AA093301.

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XX Nucleic acid encoding transforming growth factor-beta -
PT cloned into expression vectors for expression in eukaryotic host
PT cells for therapeutic use
PS Disclosure; Fig 1b; 28pp; English.
XX Pre-TGF-beta-1 is a polypeptide of 390 amino acids. Post-translational
CC cleavage of the precursor gives rise to the mature TGF-beta monomer.
CC The sequence for human TGF-beta was determined by direct amino acid
CC sequence analysis and by deduction from the TGF-beta cDNA. It is
CC capable of inducing EGF-potential anchorage-independent growth of
CC target cell lines, and/or growth inhibition of neoplastic cell lines. It
CC can be used for treating wounds, eg burns or epidermal ulcers.
SQ Sequence 390 AA:
Query Match 88.9%; Score 1919.5; DB 11; Length 390;
Best local similarity 89.7%; Pred. No. 9.9e-160;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;
QY 1 MAPSGRLRLPLPLMLVLTGPRPAAGLSTCKTIDMELVKRRIRIAIRGQILSKRLA 60
D 1 MPPSGRLRLPLPLMLVLTGPRPAAGLSTCKTIDMELVKRRIRIAIRGQILSKRLA 60
QY 61 SPPSGGVPPGRLPEAVLALYNSTRDRVAGESEVPEPEADYIAKEVTRVAVESGNOI 120
D 61 SPPSGGVPPGRLPEAVLALYNSTRDRVAGESEVPEPEADYIAKEVTRVAVESGNOI 120
QY 121 YDKFKGTPHSLVLMFNSELREAVPEPVLLSRARLRLRLKLKVEQHVLEYOKYSNDSMR 180
D 121 YDKFKQSTHSTYMFNTSELREAVPEPVLLSRARLRLRLKLKVEQHVLEYOKYSNDSMR 180
QY 181 YLSNRLAPSDSPPEWLSFDVTGVYRQMLTRRAIEGFRLSAHSSSDSKDNLTLYVEINGFN 240
D 181 YLSNRLAPSDSPPEWLSFDVTGVYRQMLTRRAIEGFRLSAHSSSDSKDNLTLYVEINGFN 240
QY 241 SGRRGDLATIHGMNRPFLLMATPLERAQHLSSRRRALDNTSPYDVPDYASLALDTN 300
D 241 TGRGDLATIHGMNRPFLLMATPLERAQHLSSRRRALDNTSPYDVPDYASLALDTN 300
QY 301 YCFSSSTEKNCCVROLYIDFRKDLGKWKIHEPKGYHANFCIGPCPYIWSLDTQYSKVLALY 360
D 284 YCFSSSTEKNCCVROLYIDFRKDLGKWKIHEPKGYHANFCIGPCPYIWSLDTQYSKVLALY 360
QY 361 NQHNPGASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 407
D 344 NQHNPGASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 6
AAR13813
AAR13813 standard; protein: 390 AA.
AAR13813:
20-NOV-1991 (first entry)
Human pro-TGF-beta 1.
Osteogenetic; tumoricidal.
Homo sapiens.
Key Location/Qualifiers
Peptide 1..29
Peptide /note="signal peptide"
Peptide 30..390
Peptide /note="pro-TGF-beta 1"
Peptide 279..390
/note="TGF-beta 1"

JP03180192-A.

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XX 06-AUG-1991.
 PD 07-DEC-1989; 89JP-0318243.
 PF 07-DEC-1989; 89JP-0318243.
 PR (KIRI) KIRIN BREWERY KK.
 PA WPI; 1991-271579/37.
 XX N-PSDB; AAQ13392.
 DR Human pro-TGF-beta 1 prodn., for osteo-genetic activity - by
 PT preparing DNA chain contg. base sequence coding for human
 PT pre-pro-TGF-beta 1, forming expression vector etc.
 XX Claim 1; Fig 1; 16pp; Japanese.
 PS The amino acid sequence codes for human prepro-TGF-beta 1 which
 CC can be produced by recombinant methods, it has osteogenetic and
 CC tumoricidal activity.
 CC
 SQ Sequence 390 AA;
 Query Match 88.9%; Score 1919.5; DB 12; Length 390;
 Best Local Similarity 89.7%; Pred. No. 9.9e-160;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;
 QY 1 MAPSGRLRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
 DB 1 MPFGLRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
 QY 61 SPSQGDVPPGPPLPEAVLALYNSTRDRAVAGESVEPEPEADYAKETRVLMVESGNOI 120
 DB 61 SPSQGEVPPGPPLPEAVLALYNSTRDRAVAGESAEBPEPEADYAKETRVLMVETHNEI 120
 QY 121 YDKRKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVQHVHLYOKYSNDSMR 180
 DB 121 YDKFKQSTHSLYMFNTSELREAVPEPVLLSRAELRLRLKLVQHVHLYOKYSNDSMR 180
 QY 181 YLSNRLAPSDSPPEWLSFDYGVVQWMLTRREAIEGFRLSAHSSSKDNTLHVEINGFN 240
 DB 181 YLSNRLAPSDSPPEWLSFDYGVVQWMLSRGIEIEGFRLSAHSCSDSRNTLQVDINGFT 240
 QY 241 SGRGDLATIHGMNRPFLLMATPLERAQHLHSSRRRALDNTSYPYDVAASLALDTN 300
 DB 241 TGRGDLATIHGMNRPFLLMATPLERAQHLHSSRRRALDNTSYPYDVAASLALDTN 300
 QY 301 YCFSTERNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKYLALY 360
 DB 284 YCFSTERNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKYLALY 343
 QY 361 NOHNPASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKS 407
 DB 344 NOHNPASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKS 390
 RESULT 7
 AAR73596
 ID AAR73596 standard; Protein: 390 AA.
 XX AAR73596;
 AC AAR73596;
 XX 20-DEC-1995 (first entry)
 DE Human TGF-beta 1 protein.
 XX
 XX Transforming growth factor-beta: Human TGF-beta protein; TGF-beta 1;
 KW TGF-beta 3; osteogenic cell source; OCS; bone deficiency;
 XX bone-inducing cofactor.
 XX Homo sapiens.
 OS

PN US5409896-A.
 PD 25-APR-1995.
 XX 12-NOV-1993; 93US-0401906.
 PF 01-SEP-1989; 89US-0401906.
 PR 12-NOV-1991; 91US-0790856.
 PR 18-MAY-1993; 93US-0063841.
 PR 12-NOV-1993; 93US-0132405.
 XX (GETH) GENENTECH INC.
 PA Ammann AJ, Rudman CG;
 PI WPI; 1995-169610/22.
 DR
 XX
 XX Compns. for treating skeletal tissue deficiency - comprising
 PT transforming growth factor-beta and an osteogenic cell source in a
 PT carrier
 PS Claim 3; Column 15-18; 19pp; English.
 XX This sequence represents human transforming growth factor-beta 1
 CC (TGF-beta 1). This sequence and the sequence for human TGF-beta 3 (see
 CC AAR73598) are claimed within the scope of the invention. The invention
 CC is a composition consisting of a TGF-beta protein and an osteogenic cell
 CC source (OCS) formulated in an acceptable carrier other than a bone
 CC morphogenic cofactor. This composition can be used for the restoration
 CC of bone deficiency. This provides for the generation of mature bone
 CC only where it is required, without the inclusion of a specific
 CC bone-inducing cofactor. This method can be used with any of the 5 human
 CC TGF-beta's or with TGF-beta from other species.
 SQ Sequence 390 AA;
 Query Match 88.9%; Score 1919.5; DB 16; Length 390;
 Best Local Similarity 89.7%; Pred. No. 9.9e-160;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;
 QY 1 MAPSGRLRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
 DB 1 MPFGLRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
 QY 61 SPSQGDVPPGPPLPEAVLALYNSTRDRAVAGESVEPEPEADYAKETRVLMVESGNOI 120
 DB 61 SPSQGEVPPGPPLPEAVLALYNSTRDRAVAGESAEBPEPEADYAKETRVLMVETHNEI 120
 QY 121 YDKRKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVQHVHLYOKYSNDSMR 180
 DB 121 YDKFKQSTHSLYMFNTSELREAVPEPVLLSRAELRLRLKLVQHVHLYOKYSNDSMR 180
 QY 181 YLSNRLAPSDSPPEWLSFDYGVVQWMLTRREAIEGFRLSAHSSSKDNTLHVEINGFN 240
 DB 181 YLSNRLAPSDSPPEWLSFDYGVVQWMLSRGIEIEGFRLSAHSCSDSRNTLQVDINGFT 240
 QY 241 SGRGDLATIHGMNRPFLLMATPLERAQHLHSSRRRALDNTSYPYDVAASLALDTN 300
 DB 241 TGRGDLATIHGMNRPFLLMATPLERAQHLHSSRRRALDNTSYPYDVAASLALDTN 300
 QY 301 YCFSTERNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKYLALY 360
 DB 284 YCFSTERNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKYLALY 343
 QY 361 NOHNPASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKS 407
 DB 344 NOHNPASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKS 390
 RESULT 8
 AAR90827
 ID AAR90827 standard; Protein: 390 AA.
 XX

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AC AAR90827;
XX
XX 25-JAN-1980 (first entry)
XX
XX Pre-transforming growth factor beta 1.
XX
XX transforming growth factor beta 1; wound healing;
XX recombinant production.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 8..23
XX /note= "hydrophobic domain"
XX Modified-site 82..84
XX /note= "potential N-glycosylation site"
XX Modified-site 136..138
XX /note= "potential N-glycosylation site"
XX Modified-site 176..178
XX /note= "potential N-glycosylation site"
XX Cleavage-site 277..279
XX /note= "trypsin-like peptidase cleavage site"
XX Protein 279..390
XX /label= mature_TGF_beta_1
XX
XX US5482851-A.
XX
XX 09-JAN-1996.
XX
XX 22-MAR-1985; 85US-0715142.
XX
XX 13-MAR-1987; 87US-0025423.
XX 22-MAR-1985; 85US-0715142.
XX 04-AUG-1989; 89US-0389929.
XX 04-MAR-1992; 92US-0845893.
XX 05-NOV-1993; 93US-0147364.
XX
XX (GETH ) GENENTECH INC.
XX
XX Derynck RMA, Goeddel DV;
XX
XX MPI: 1996-076891/08.
XX N-PSDB; AAT15720.
XX
XX New recombinant human transforming growth factor-beta prods. - produced
XX using Chinese hamster ovary cells, for use in diagnostic applications
XX or in therapy
XX
XX Example 3; Fig 1A-C; 26pp; English.
XX
XX The pre-transforming growth factor (TGF) beta 1 protein is encoded
XX by AAT15720. The mature TGF beta 1 monomer is cleaved from the
XX precursor at the Arg-Arg dipeptide immediately preceding the mature
XX TGF-beta 1 NH2-terminus. It does not contain a recognisable N-terminal
XX signal peptide typical of most secreted proteins. The pre-TGF beta 1
XX contains several pairs of basic residues which could undergo
XX post-translational cleavage and give rise to separate polypeptide
XX entities. The precursor contains 3 potential N-glycosylation sites, none
XX of which are localised in the mature TGF beta 1. This is useful in
XX purification of the mature protein. TGF beta 1 can be used in, e.g. wound
XX healing.
XX
XX Sequence 390 AA:

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Db 61 SPPSQGEVPEGPPLPEAVLALYNSTRDRVAGESAPEPEPEADYAAKEVRLVMEVTHNEI 120
QY 121 YDKFKGTPHSLYMLFNTSELEAVEPEVLLSRAELRLRLKLVQEHVELYOKYSNDSMR 180
Db 121 YDKFKGTPHSLYMLFNTSELEAVEPEVLLSRAELRLRLKLVQEHVELYOKYSNDSMR 180
QY 181 YLSNRLAPSDSPPELSDVGVVROWLRRRAITGEFRLSAHSSSSSKDNTLHVEINGFN 240
Db 181 YLSNRLAPSDSPPELSDVGVVROWLRRRAITGEFRLSAHSSSSSKDNTLHVEINGFN 240
QY 241 SGRRGDLATTIGMNRPELLMATPLERAQHLHSSRRRAALDNTNSPYDVEDYASALDTN 300
Db 241 TGRRGDLATTIGMNRPELLMATPLERAQHLHSSRRRAALDNTNSPYDVEDYASALDTN 300
QY 301 YCFSESTERKNCVROLYIDFRDGLGKWKIHEPKGYHANFCLGCPYIWSLDTOYSKVALY 360
Db 284 YCFSESTERKNCVROLYIDFRDGLGKWKIHEPKGYHANFCLGCPYIWSLDTOYSKVALY 343
QY 361 NQHNPGASAPCCVQALPEPLIYVYVGRKPKVEQLSNMIVRSCKS 407
Db 344 NQHNPGASAPCCVQALPEPLIYVYVGRKPKVEQLSNMIVRSCKS 390

RESULT 9
AAU77101
ID AAU77101 standard; Protein; 390 AA.
XX
XX AAU77101.
XX
XX 05-JUN-2002 (first entry)
XX
XX Human transforming growth factor beta 1 (TGF-beta-1) polypeptide.
XX
XX Human: transforming growth factor beta; TGF-beta; insulin production;
XX type I diabetes mellitus; pancreatic cell outgrowth; wound healing;
XX pancreatic duct tissue; ischaemia; stroke; nervous system aging;
XX neurological condition; neurodegenerative disease; inflammation;
XX vascular injury; chemical injury; traumatic injury; tumour-induced injury;
XX amyotrophic lateral sclerosis; spinocerebellar degeneration;
XX immunological disease; multiple sclerosis; TGF-beta-1.
XX
XX Homo sapiens.
XX
XX MO200212336-A2.
XX
XX 14-FEB-2002.
XX
XX 09-FEB-2001; 2001WO-US04192.
XX
XX 09-AUG-2000; 2000US-0635368.
XX
XX (CUR1-) CURIS INC.
XX
XX Wang M, Pang K;
XX
XX MPI: 2002-257468/30.
XX
XX Treating a subject with a disorder resulting from insufficient insulin
XX production, and inducing outgrowth of pancreatic cells, involves using
XX a transforming growth factor beta therapeutic
XX
XX Disclosure; Fig 1; 77pp; English.
XX
XX The invention relates to treating a subject with a disorder resulting
XX from insufficient insulin production, involving contacting the subject
XX with a transforming growth factor beta (TGF-beta) therapeutic. TGF-beta
XX polypeptides can be used for treating a subject with a disorder resulting
XX from insufficient insulin production, e.g. type I diabetes mellitus, and
XX for inducing outgrowth of pancreatic cells associated with pancreatic
XX duct tissue within a subject. A composition comprising a TGF-beta protein
XX may be useful in wound healing and treatment of neurological conditions
XX derived from acute, subacute or chronic injury to the nervous system,

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CC including traumatic injury, chemical injury, vascular injury and deficits (such as ischemia resulting from stroke), together with
 CC infectious/inflammatory and tumor-induced injury, aging of the nervous
 CC system including Alzheimer's disease, chronic neurodegenerative diseases
 CC including Parkinson's disease, Huntington's chorea, amyotrophic lateral
 CC sclerosis, spinocerebellar degeneration and chronic immunological
 CC diseases of the nervous system or affecting the nervous system, including
 CC multiple sclerosis. This sequence represents the human TGF-beta-1
 CC protein.
 XX
 CC
 XX Sequence 390 AA:
 SQ
 Query Match 88.8%; Score 1916.5; DB 23; Length 390;
 Best Local Similarity 89.7%; Pred. No. 1.8e-159;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;
 QY 1 MAPSGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRIEAIHQIISKRLA 60
 DB 1 MPSPGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRIEAIHQIISKRLA 60
 QY 61 SPSPGQVPPGPIPEAVLALYNSTRDRAVAGSEVPEPEADYAKETRYLMVWESGNOI 120
 DB 61 SPSPGQVPPGPIPEAVLALYNSTRDRAVAGSEVPEPEADYAKETRYLMVWESGNOI 120
 QY 121 YDFKGPHTSLYMLFNTSELREAVPEPVLSRAELRLRLKLYEQHVELYOKYSNDSMR 180
 DB 121 YDFKGPHTSLYMLFNTSELREAVPEPVLSRAELRLRLKLYEQHVELYOKYSNDSMR 180
 QY 181 YLSNRLIAPSDSPWLSFDYTGVRQWLTREAEIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 DB 181 YLSNRLIAPSDSPWLSFDYTGVRQWLTREAEIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 QY 241 SGRGDLATIHGMNRPFLMLATPLERAQHLSSRHRRALDTNSYPVVPYASALADTN 300
 DB 241 TGRGDLATIHGMNRPFLMLATPLERAQHLSSRHRRALDTNSYPVVPYASALADTN 300
 QY 301 YCFSTERNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGPCPYIWSLDIQYSKVLA 360
 DB 284 YCFSTERNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGPCPYIWSLDIQYSKVLA 343
 QY 361 NQHNPGASAPCCVQALPELPYIYVGRKPKVEQLSMNIYRSCKCS 407
 DB 344 NQHNPGASAPCCVQALPELPYIYVGRKPKVEQLSMNIYRSCKCS 390
 RESULT 10
 AEI6943
 ID AEI6943 standard; Protein: 390 AA.
 XX
 XX AEI6943;
 DT 18-APR-2002 (first entry)
 DE Human transforming growth factor-beta1 (TGF-beta1) protein.
 XX
 XX Human: transforming growth factor-beta1; TGF-beta1; osteoporosis;
 KW latency associated peptide; LAP; integrin alphavbeta3; apoptosis;
 KW immunomodulation; inflammatory disease; fibrotic disease; cancer;
 KW diabetic retinopathy; chronic obstructive pulmonary disorder;
 KW bone resorption; rheumatoid arthritis; psoriasis; restenosis;
 KW atherosclerosis; liver fibrosis; asthma; cytoskeletal; osteopathic;
 KW ophthalmological; antiarteriosclerotic; vasotropic.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..29
 FT Region /label= "Signal-peptide
 FT 30..278
 FT Domain /note= "LAP-beta1"
 FT 244..246
 FT /note= "RGD motif"
 FT 279..390
 FT Protein

FT /note= "Human mature TGF-beta1 protein"
 XX
 XX W0200190186-A1.
 XX
 XX 29-NOV-2001.
 PD
 XX
 XX 25-MAY-2001; 2001WO-GB02352.
 PF
 XX 26-MAY-2000; 2000GB-0012991.
 PR 05-JAN-2001; 2001GB-0000286.
 XX
 XX (GLAX) GLAXO GROUP LTD.
 PA
 XX Ludbrook S, Barry S, Horgan C, Miller D;
 PI WPI; 2002-097645/13.
 DR
 XX
 XX Identifying modulators of interactions between latency associated
 PT peptides and integrin alphavbeta3 for therapeutics, by contacting the
 PT peptide and integrin with a test product and determining if the product
 PT modulates interaction -
 XX
 XX Disclosure; Page 37-39; 44pp; English.
 PS
 XX
 XX The invention relates to a method for identification of a modulator
 CC of the interaction between latency associated peptide (LAP) of
 CC transforming growth factor-beta1 (TGF-beta1) and integrin alphavbeta3.
 CC The method is useful for identifying a modulator of the interaction
 CC between LAP and integrin alphavbeta3. The method is useful for
 CC immunomodulation, in the treatment of inflammatory disease, fibrotic
 CC disease, cancer, diabetic retinopathy, bone resorption or osteoporosis,
 CC and for preventing apoptosis administering the modulator to the host.
 CC The modulator (inhibitor of the interaction between LAP-beta1 and
 CC integrin alphavbeta3) is useful in the manufacture of a medicament for
 CC immunomodulation. The modulator (activator of the interaction between
 CC LAP-beta1 and integrin alphavbeta3) is useful in the manufacture of
 CC medicament for preventing apoptosis. The modulator is useful for
 CC treating a inflammatory or fibrotic disease such as chronic obstructive
 CC pulmonary disorder, rheumatoid arthritis, psoriasis, restenosis,
 CC atherosclerosis, liver fibrosis and asthma. The present sequence is
 CC human TGF-beta1 protein.
 XX
 XX
 SQ Sequence 390 AA:
 Query Match 88.8%; Score 1916.5; DB 23; Length 390;
 Best Local Similarity 89.7%; Pred. No. 1.8e-159;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;
 QY 1 MAPSGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRIEAIHQIISKRLA 60
 DB 1 MPSPGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRIEAIHQIISKRLA 60
 QY 61 SPSPGQVPPGPIPEAVLALYNSTRDRAVAGSEVPEPEADYAKETRYLMVWESGNOI 120
 DB 61 SPSPGQVPPGPIPEAVLALYNSTRDRAVAGSEVPEPEADYAKETRYLMVWESGNOI 120
 QY 121 YDFKGPHTSLYMLFNTSELREAVPEPVLSRAELRLRLKLYEQHVELYOKYSNDSMR 180
 DB 121 YDFKGPHTSLYMLFNTSELREAVPEPVLSRAELRLRLKLYEQHVELYOKYSNDSMR 180
 QY 181 YLSNRLIAPSDSPWLSFDYTGVRQWLTREAEIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 DB 181 YLSNRLIAPSDSPWLSFDYTGVRQWLTREAEIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 QY 241 SGRGDLATIHGMNRPFLMLATPLERAQHLSSRHRRALDTNSYPVVPYASALADTN 300
 DB 241 TGRGDLATIHGMNRPFLMLATPLERAQHLSSRHRRALDTNSYPVVPYASALADTN 300
 QY 301 YCFSTERNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGPCPYIWSLDIQYSKVLA 360
 DB 284 YCFSTERNCCVROLYIDFRKDLGKWIHEPKGYHANFCLGPCPYIWSLDIQYSKVLA 343
 QY 361 NQHNPGASAPCCVQALPELPYIYVGRKPKVEQLSMNIYRSCKCS 407

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Db 344 NOHNPASAAAPCCVQALPEPLPIVYVGRKPKVEQLSNMIVRSCKS 390
|||||
RESULT 11
ID AAR20124 standard; Protein; 390 AA.
XX AAR20124;
XX AC
XX DT 16-APR-1992 (first entry)
XX DE
XX KW Sequence of simian transforming growth factor (TGF) beta-1.
XX HT Hypertension therapy; hypotensive agent; blood pressure modulator.
XX OS Monkey.
XX FT Key Location/Qualifiers
XX FT Peptide 8..21
XX FT Protein 279..390
XX PN MO9119513-A.
XX PD 26-DEC-1991.
XX PE 20-JUN-1991; 91WO-0504449.
XX PR 20-JUN-1990; 90US-0541221.
XX RA (BRIM ) BRISTOL-MYERS SQUIB.
XX PI Oleson FB, Comerreski CR;
XX DR MPI; 1992-024199/03.
XX DR N-PSDB; AAQ20289.
XX PT Use of transforming growth factor (TGF)-beta and their
XX PT antagonists - for modulating blood pressure, for treating
XX PT hypertension and hypotension
XX PS
XX PS Disclosure; Fig 1; 42pp; English.
CC A new method for treating hypertension comprises administering a
CC transforming growth factor (TGF)-beta to an individual at a dose
CC effective for lowering blood pressure; the TGF-beta may be e.g.
CC mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
CC beta1 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
CC beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
CC complex.
XX
XX Sequence 390 AA:
SQ
Query Match 88.7%; Score 1914.5; DB 13; Length 390;
Best Local Similarity 89.4%; Pred. No. 2.7e-159;
Matches 364; Conservative 10; Mismatches 16; Indels 17; Gaps 1;
QY 1 MAPSGRLRLPLPLMLVLTGPRPAGLSTCKTIDMLVKKRIEIRGILSKRLA 60
| : |||
DB 1 MPSPGRLRLPLPLMLVLTGPRPAGLSTCKTIDMLVKKRIEIRGILSKRLA 60
| : |||
QY 61 SPSPGQDVPRGPPEALVALYNSRDRVAGSEVPEPEADYVAKETRVLMVESGNCI 120
| : |||
DB 61 SPSPGQDVPRGPPEALVALYNSRDRVAGSEVPEPEADYVAKETRVLMVESGNCI 120
| : |||
QY 121 YDKFKCTPHSLMLFNTSELREAVPEPVLISRAELRLRLKLVQHOHELXOKYSNDSWR 180
| : |||
DB 121 YDKFKCTPHSLMLFNTSELREAVPEPVLISRAELRLRLKLVQHOHELXOKYSNDSWR 180
| : |||
QY 181 YLSNRLIAPSDSEPMWLSFDYTGVRQWLTTRREAIEGFRLSAHSSSDSKNDTLHVEITGFN 240
| : |||
DB 181 YLSNRLIAPSDSEPMWLSFDYTGVRQWLTTRREAIEGFRLSAHSSSDSKNDTLHVEITGFN 240
| : |||

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```

QY 241 SGRGDIATIHGMNRPPELLMATPLERAQHLSSRRRALDTNTPYDVPDYASIALDTN 300
| : |||
DB 241 TGRGDIATIHGMNRPPELLMATPLERAQHLSSRRRALDTNTPYDVPDYASIALDTN 300
| : |||
QY 301 YCFSSTEKNCVROLYTIDERRDLGKWKIHEPKGYHANPCIGPCPYTWSLDTQSKYVALY 360
| : |||
DB 284 YCFSSTEKNCVROLYTIDERRDLGKWKIHEPKGYHANPCIGPCPYTWSLDTQSKYVALY 360
| : |||
QY 361 NOHNPASAAAPCCVQALPEPLPIVYVGRKPKVEQLSNMIVRSCKS 407
| : |||
DB 344 NOHNPASAAAPCCVQALPEPLPIVYVGRKPKVEQLSNMIVRSCKS 390
| : |||
RESULT 12
ID AAR46227 standard; Protein; 390 AA.
XX AAR46227;
XX AC
XX DT 09-JUL-1994 (first entry)
XX DE
XX KW Human pre-TGF-beta-1.
XX HT TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
XX KW transforming growth factor beta-3; recombinant; wound healing;
XX KW vulnerable.
XX OS Homo sapiens.
XX FT Key Location/Qualifiers
XX FT Peptide 279..390
XX FT /label= Mat-peptide
XX FT 279
XX FT /note= "TGF-beta-1 release site"
XX FT 82..84
XX FT /label= N-glycosylation_site
XX FT 136..138
XX FT /label= N-glycosylation_site
XX FT 176..178
XX FT /label= N-glycosylation_site
XX PN
XX PD US5284763-A.
XX PE 08-FEB-1994.
XX PF 22-MAR-1985; 85US-0715142.
XX PR 22-MAR-1985; 85US-0715142.
XX PR 13-MAR-1987; 87US-0025423.
XX PR 04-AUG-1989; 89US-0389929.
XX PR 04-MAR-1992; 92US-0845893.
XX PA (GETH ) GENENTECH INC.
XX PI Derynk RMA, Goeddel DV;
XX PI MPI; 1994-056343/07.
XX DR N-PSDB; AAQ56923.
XX PT Nucleic acid sequences encoding transforming growth factor-beta -
XX PT diagnostic probes, and for use in therapeutics
XX PS
XX PS Disclosure; Fig 1b; 25pp; English.
XX CC cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
XX CC p19 TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
XX CC corresponding amino acid sequences were determined (AAR46227-29,
XX CC respectively). A genomic fragment corresponding to a human TGF-
XX CC beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
XX CC determined (AAR46230). The sequences have been used in the
XX CC construction of vectors for the expression of recombinant TGF-
XX CC beta.

```

SQ Sequence 390 AA:
 Query Match 88.5%; Score 1910.5; DB 15; Length 390;
 Best Local Similarity 89.4%; Pred. No. 6.1e-159;
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 D 1 MPPSGRLRLPLPLMLLVLTGPRPAGLSTCKTIMELVKKRIEAIKQILSKRLA 60
 QY 61 SPPSGDVPPEGPLPEAVLALYNSTRDVAGSVEPEPEADYAKETRVLMVSGNQI 120
 D 61 SPPSGDVPPEGPLPEAVLALYNSTRDVAGSVEPEPEADYAKETRVLMVSGNQI 120
 QY 121 YDFKGTGPHSLYMLFNTSELREAVPEPVLSRAELRLRLKLVQEHVLYOKYSNDSWR 180
 D 121 YDFKGTGPHSLYMLFNTSELREAVPEPVLSRAELRLRLKLVQEHVLYOKYSNDSWR 180
 QY 181 YLSNRLAPSDSPFWLSFDVYGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 D 181 YLSNRLAPSDSPFWLSFDVYGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 QY 241 SGRGDLATIHGMNRPFLMLMATPLERAQHLSSRRRALDNTSYPDVYASIALDNTN 300
 D 241 TGRGDLATIHGMNRPFLMLMATPLERAQHLSSRRRALDNTSYPDVYASIALDNTN 300
 QY 301 YCFSTEKNCVCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTOYSKVYALY 360
 D 284 YCFSTEKNCVCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTOYSKVYALY 343
 QY 361 YQHNPGASAPCCVPQALEPLPIYVYVGRKPKVQQLSNMIVRSCKCS 407
 D 344 YQHNPGASAPCCVPQALEPLPIYVYVGRKPKVQQLSNMIVRSCKCS 390
 Db 344 YQHNPGASAPCCVPQALEPLPIYVYVGRKPKVQQLSNMIVRSCKCS 390
 RESULT 13
 AAR83054
 ID AAR83054 standard; Protein; 391 AA.
 AC AAR83054;
 DT 25-JUN-1996 (first entry)
 DE Transforming growth factor-beta 1.
 KW macrophage inducible nitric oxide synthase; iNOS; constitutive NOS; interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta; nitric oxide production; hypotension; inflammation; septic shock;
 KM nitric oxide production; hypotension; inflammation; septic shock;
 OS Mammalian sp.
 FH Key Location/Qualifiers
 FT Protein 279..391
 FT /note="represents the mature active TGF beta-1 mol."
 W09526745-A1.
 PD 12-OCT-1995.
 PE 05-APR-1994; 94WO-US03705.
 PR 05-APR-1994; 94WO-US03705.
 PA (HARD) HARVARD COLLEGE.
 PI Lee M, Perrella MA;
 PI WPI; 1995-358443/46.
 DR N-PSDB; AAT05876.
 PT Treatment of hypotension, esp. in septic shock - by administering transforming growth factor-beta e.g. to inhibit inducible nitric

PT oxide synthase gene transcription
 PS Disclosure; Fig 17; 52pp; English.
 CC Transforming growth factor-beta 1 (TGF-beta 1) has been found to inhibit
 CC inducible nitric oxide synthase (iNOS) gene transcription, esp. in
 CC interleukin-1-beta (IL1-beta) stimulated rat smooth muscle cells, and at
 CC a dose which does not inhibit constitutive NOS. TGF-beta 1 or 2
 CC (AAR83055) or their active fragments (esp. derived from the
 CC carboxy-terminal 112 amino acids), can be used in the treatment of
 CC hypotension, such as that associated with severe inflammation or septic
 CC shock.
 XX
 SQ Sequence 391 AA:
 Query Match 88.4%; Score 1909; DB 16; Length 391;
 Best Local Similarity 89.5%; Pred. No. 8.3e-159;
 Matches 365; Conservative 10; Mismatches 15; Indels 18; Gaps 2;
 QY 1 MAPSGRLRLPLPLMLLVLTGPRPAGLSTCKTIMELVKKRIEAIKQILSKRLA 60
 D 1 MPPSGRLRLPLPLMLLVLTGPRPAGLSTCKTIMELVKKRIEAIKQILSKRLA 60
 QY 61 SPPSGDVPPEGPLPEAVLALYNSTRDVAGSVEPEPEADYAKETRVLMVSGNQI 120
 D 61 SPPSGDVPPEGPLPEAVLALYNSTRDVAGSVEPEPEADYAKETRVLMVSGNQI 120
 QY 121 YDFKGTGPHSLYMLFNTSELREAVPEPVLSRAELRLRLKLVQEHVLYOKYSNDSW 179
 D 121 YDFKGTGPHSLYMLFNTSELREAVPEPVLSRAELRLRLKLVQEHVLYOKYSNDSW 180
 QY 180 YLSNRLAPSDSPFWLSFDVYGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 239
 D 181 YLSNRLAPSDSPFWLSFDVYGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 QY 240 NSGRGDLATIHGMNRPFLMLMATPLERAQHLSSRRRALDNTSYPDVYASIALDNT 299
 D 241 TGRGDLATIHGMNRPFLMLMATPLERAQHLSSRRRALDNTSYPDVYASIALDNT 283
 QY 300 NYCFSTEKNCVCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTOYSKVYALY 359
 D 284 NYCFSTEKNCVCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTOYSKVYALY 343
 QY 360 YQHNPGASAPCCVPQALEPLPIYVYVGRKPKVQQLSNMIVRSCKCS 407
 D 344 YQHNPGASAPCCVPQALEPLPIYVYVGRKPKVQQLSNMIVRSCKCS 391
 RESULT 14
 AAW78785
 ID AAW78785 standard; Protein; 390 AA.
 AC AAW78785;
 DT 21-DEC-1998 (first entry)
 DE Human pre-transforming growth factor-beta 1.
 KW Transforming growth factor-beta 1; TGF-beta 1; human.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 8..23
 FT Protein 279..390
 FT /note="hydrophobic domain"
 FT /label=Mat_protein
 FT Modified-site 82..84
 FT /note="Asn is N-glycosylated"
 FT Modified-site 136..138
 FT /note="Asn is N-glycosylated"
 FT Modified-site 176..178
 FT /note="Asn is N-glycosylated"

FT	Cleavage site	277..278	/note= "cleavage site for release of TGF-beta 1"
FT	US5801231-A.		
XX	01-SEP-1998.		
XX	22-MAR-1985.	85US-0715142.	
XX	13-MAR-1987.	87US-0025423.	
PR	22-MAR-1985.	85US-0715142.	
PR	04-AUG-1989.	89US-0389929.	
PR	04-MAR-1992.	92US-0845893.	
PR	05-NOV-1993.	93US-0147364.	
PR	30-MAY-1995.	95US-0454468.	
XX	(GETH) GENENTECH INC.		
PA	Derynck RMA, Goeddel DV;		
XX	MP1: 1998-494840/42.		
DR	N-PSDB: AAV52933.		
XX	DNA encoding transforming growth factor-beta precursor sequence -		
PT	useful for analysis to perform manipulations to increase yield of		
PT	recombinant production of the protein		
XX	Example 3; Fig 1B 1-3; 26pp: English.		
CC	This is the amino acid sequence of human transforming growth		
CC	factor-beta 1 precursor (preTGF-beta 1). It was deduced from		
CC	a preTGF-beta 1 cDNA sequence (see AAV52933). The invention relates		
CC	to the recombinant production of TGF-beta. Biologically active		
CC	TGF-beta is defined as being capable of inducing EGF-potentiated		
CC	anchorage independent growth of target cell lines and/or growth		
CC	inhibition of neoplastic cell lines. Nucleic acids encoding		
CC	TGF-beta have been isolated and cloned into vectors which are		
CC	replicated in bacteria and expressed in eukaryotic cells. TGF-beta		
CC	recovered from transformed cells is used in known therapeutic		
CC	applications.		
XX	Sequence 390 AA;		
XX	Query Match 88.4%; Score 1908.5; DB 19; Length 390;		
XX	Best Local Similarity 89.2%; Pred. No. 9.1e-159;		
XX	Matches 363; Conservative 10; Mismatches 17; Indels 17; Gaps		
QY	1 MARGRLRLPLLLPLMLVLTPGRPAAGLSTCKTIDMELVKKRRIARIGQILSKRLA 60		
DB	1 MPBGLRLPLLLPLMLVLTPGPAPALSTCKTIDMEVKKRRIARINQILSKRLA 60		
QY	61 SPPSGDVPPLPAVALALYNSTRVRVAGESEVEPEPEADYAKAEYTRLVNYESGNOI 120		
DB	61 SPPSGEVPPLPAVALALYNSTRVRVAGESAEPEPEADYAKAEYTRLVNETHNEI 120		
QY	121 YDKRGKTPHSLYMLFNTSELREAVEPEVLLSRAELRLRLKLVQEHVELYQKYSNDSMR 180		
DB	121 YDKRKQSHSLYMLFNTSELREAVEPEVLLSRAELRLRLKLVQEHVELYQKYSNDSMR 180		
QY	181 YLSNRLAPSDSEPMWLFSDVGTGVVROWLTRREAIEGFRLSAHSSSDSKNTLHVEINFPN 240		
DB	181 YLSNRLAPSDSEPMWLFSDVGTGVVROWLTRREAIEGFRLSAHSCSDSKNTLQVDINGFT 240		
QY	241 SGRGGLATITGHMNPFLILMATPLERAQHLSRRHRRALDNTNYPYDVPYASIALDTN 300		
DB	241 TGRGGLATITGHMNPFLILMATPLERAQHLSRRHRRALDNTNYPYDVPYASIALDTN 300		
QY	301 YCFSSSTENCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPCPYIWSLDTQYSKVALY 360		
DB	284 YCFSSSTENCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPCPYIWSLDTQYSKVALY 343		
QY	361 NQHPNGASAPCCVDALEPLPIVYVYVGRKKVEQLSNMIVRSCKS 407		

Db	344	NQHNPGASAPCCVPOALEPLIVYVGRKKVEQLSNMIVRSCKS	390
RESULT#	15		
ID	AAB84601		
XX	AAB84601 standard; Protein; 390 AA.		
XX			
AC	AAB84601;		
XX			
DT	05-SEP-2001 (first entry)		
XX			
DE	Nucleotide sequence of transforming growth factor-beta.		
XX			
XX	Growth factor; protein inhibitor; protease; damaged tissue;		
KW	platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;		
KW	keratinocyte-tissue derived growth factor; CTGF; chrysalin; VEGF;		
KW	keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;		
KW	transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;		
KW	granulocyte macrophage colony stimulating factor; GM-CSF; uPA;		
KW	vascular endothelial growth factor; urokinase plasminogen activator;		
KW	dermal ulcer; wound.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference 159	/note= "Arg encoded by AGGAGC"	
FT	Misc-difference 321	/note= "Cys encoded by TTC"	
FT	Misc-difference 378	/note= "Glu encoded by CAG"	
FT			
XX			
PN	WO200149309-A2.		
XX			
PD	12-JUL-2001.		
PF	21-DEC-2000; 2000MO-IB01935.		
XX			
PR	29-DEC-1999; 99GB-0030768.		
PA	(PF12) PFIZER LTD.		
PA	(PF12) PFIZER INC.		
XX			
PI	Davies MJ, Huggins JP, McIntosh FS, Occleston NL;		
XX			
DR	WPI: 2001-418351/44.		
XX			
DR	N-PsDB; AAH28216.		
XX			
PT	Composition for the treatment of damaged tissue i.e. chronic wounds and		
PT	dermal ulcers comprises an inhibitor agent i.e. a protease and a growth		
PT	factor -		
XX			
PS	Disclosure; Page 547; 572pp; English.		
XX			
CC	The specification describes a pharmaceutical composition, comprising		
CC	a growth factor, an inhibitor agent, i.e. a protease. The inhibitor		
CC	agent inhibits the action of at least one specific adverse protein,		
CC	i.e. a protease, that is upregulated in a damaged tissue such as a		
CC	wound environment. Growth factors which are included in the composition		
CC	of the invention are platelet-derived growth factor (PDGF), fibroblast		
CC	growth factor (FGF), connective tissue derived growth factor (CTGF),		
CC	keratinocyte-derived growth factor (KGF), transforming growth		
CC	factor-beta (TGF-beta), granulocyte macrophage colony stimulating factor		
CC	(GM-CSF), epidermal growth factor (EGF), vascular endothelial growth		
CC	factor (VEGF), and chrysalin. Inhibitors which are included in the		
CC	composition of the invention include inhibitors of urokinase-type		
CC	plasminogen activator (uPA) and matrix metalloproteinase (MMP). The		
CC	composition is useful for the treatment of chronic damaged tissue, i.e.		
CC	wounds and dermal ulcers. The present sequence represents a human		
CC	TGF-beta, and is used to produce the composition of the invention.		
XX			
SQ	Sequence 390 AA;		

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 10:08:23 ; Search time 3935 Seconds
(without alignments)
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Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rtd:*
36: em_hlg_mam:*
37: em_hlg_vrt:*
38: em_sy:*
39: em_hlg_hum:*
40: em_hlg_mus:*
41: em_hlg_others:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1221.2	89.7	3306	4	PICITGBF1A
2	1211.8	89.0	1326	4	AX338213
3	1201.8	88.3	1750	4	GGTGFBI
4	1131.6	83.1	1605	4	STGFBR
5	1110.2	81.6	2221	4	AF461808
6	990.6	72.8	1369	4	DCGTGFBI
7	979.6	72.0	2527	6	E00973
8	978.8	71.9	2537	6	A06669
9	972.8	71.5	1733	4	OMTGFBI
10	972.4	71.4	1780	9	BC000125
11	972.4	71.4	1780	9	BC001180
12	971	71.3	1561	9	AGMTGFB
13	968.2	71.1	1821	6	E03028
14	967.8	71.1	1746	9	BC022242
15	966.6	71.0	1560	6	I06216
16	965.8	71.0	2745	9	HSTGFBI
17	964.6	70.9	1560	6	I08268
18	947.2	69.6	1569	6	I06221
19	942.2	69.2	1561	6	I08275
20	918.4	67.5	1173	4	ECRGFBI
21	916.6	67.3	1176	6	AX481432
22	912	67.0	1187	4	AF175709
23	889.2	65.3	1597	10	AF191297
24	860.8	63.2	1641	10	BC013738
25	847	62.2	1579	10	MUSTGFRNA
26	847	62.2	2094	10	MMU009862
27	827.4	60.8	1585	10	RMTGFB1
28	815.6	59.9	1117	4	BOVTGFB
29	791	58.1	1125	10	AF480858
30	682.2	50.1	1675	6	I03310
31	543.6	39.9	699	6	I05434
32	357.6	26.3	650	9	AX336646
33	357.6	26.3	650	9	HUMTGFBI
34	357.6	26.3	862	6	I03312
35	354.4	26.0	489	6	AX455100
36	327.2	24.0	469	10	NATGFB1
37	318.2	23.4	1256	5	CHRTGFB4
38	310.2	22.8	339	6	AR036686
39	308.6	22.7	339	4	OCFA000133
40	308.6	22.7	339	6	A18277
41	308.6	22.7	339	6	A23751
42	308.6	22.7	339	6	A48549
43	308.6	22.7	339	6	A48563
44	308.6	22.7	339	6	I56854
45	308.2	22.6	337	6	AR198575

ALIGNMENTS

RESULT 1
LOCUS PICITGBF1A
DEFINITION Sus scrofa transforming growth factor beta-1 mRNA, complete cds.
ACCESSION M23703
VERSION M23703.1 GI:755044
KEYWORDS transforming growth factor-beta-1.
SOURCE Sus scrofa (strain miniature swine) CDNA to mRNA.
ORANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 3206)
AUTHORS Kondaliah, P., Van Obberghen-Schilling, E., Ludwig, R. L., Dhar, R.,
Sporn, M. B. and Roberts, A. B.
TITLE CDNA cloning of porcine transforming growth factor-beta 1 mRNAs.

FEATURES
source Location/Qualifiers
1..1326 /organism="Sus scrofa"
/db_xref="taxon:9823"
16..1188 /note="unbanned protein product"
/codon_start=1
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/translation="MAPSGRLPLPLPLMLVLVTPRPAAGLSTCKTIDMELVKR
/RLEAIRGOLISKLRLASPPSGDVPPLPEAVLALYNSTRDVRAGSVEPEPEAD
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LSHVESDSDKNDTLHVEINENSGRDLTLTHOMNRPFLIMATPLERAOHLSSRL
RRALDNNYCSSTKNCCKRQLYIDFRKDLGKWHIEPKGHANFCUPEPTIYSLDT
QYKVLALYQNHNPASAPCCVQALEPLPIYVYVGRKPEVQLSNMIVRSKCS"

BASE COUNT 263 a 438 c 392 g 233 t

ORIGIN

Query Match 89.0%; Score 1211.8; DB 6; Length 1326;
Best Local Similarity 95.6%; Pred. No. 1,4e-209;
Matches 1299; Conservative 0; Mismatches 7; Indels 53; Gaps 3;

1 TGGACCGAGATGGGCGCTTGGGGGCTGGGCTCTTGGCGCTGCTGCGCGCTGTG 60
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6 TGGACCGAGATGGGCGCTTGGGGGCTGGGCTCTTGGCGCTGCTGCGCGCTGTG 65
|||||
61 GCTCTAGTGTGACGCTTGGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTG 120
|||||
66 GCTCTAGTGTGACGCTTGGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTG 125
|||||
121 CATGAGCTGTGAAGCGGAGCGCATGGAGGCGATTCGCGCGCGAGATTCTGTCAGCT 180
|||||
126 CATGAGCTGTGAAGCGGAGCGCATGGAGGCGATTCGCGCGCGAGATTCTGTCAGCT 185
|||||
181 TCGGCTTGGCG 240
|||||
186 TCGGCTTGGCG 245
|||||
241 ACTGCTCTTTACACAGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
|||||
246 ACTGCTCTTTACACAGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 305
|||||
301 CGAGCGAGAGCGGAGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
|||||
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|||||
361 CAACCAATCTATGATTAATTCAGGGGCAACCGCGCGCGCGCGCGCGCGCGCGCG 420
|||||
366 CAACCAATCTATGATTAATTCAGGGGCAACCGCGCGCGCGCGCGCGCGCGCGCG 425
|||||
421 GTCGAGCTCCCGGGAAGCGGTGGCGGAGCTGTATGCTCTCTCGGCGAGAGTGGCCT 480
|||||
426 GTCGAGCTCCCGGGAAGCGGTGGCGGAGCTGTATGCTCTCTCGGCGAGAGTGGCCT 485
|||||
481 GCTGAGGCTCAAGTTAAAGTGGAGCGACGCTGAGAGCTATACCAAAATACAGCAATGA 540
|||||
486 GCTGAGGCTCAAGTTAAAGTGGAGCGACGCTGAGAGCTATACCAAAATACAGCAATGA 545
|||||
541 TTTCTGGCGCTTACGACACCGGCTGCTGGCGCGCGCGCGCGCGCGCGCGCGCG 600
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546 TTTCTGGCGCTTACGACACCGGCTGCTGGCGCGCGCGCGCGCGCGCGCGCGCG 605
|||||
601 CTTTGTATGTCACGGAGTTGTGGCGAGTGGCTGAGACCGCGAGAGGCTATAGAGGTTT 660
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606 CTTTGTATGTCACGGAGTTGTGGCGAGTGGCTGAGACCGCGAGAGGCTATAGAGGTTT 665
|||||
661 TCGCCTCAGTGCCCACTCTTCTGTGACAGCAAAAGATTAACACTCCAGTGAATTTAA 720
|||||
666 TCGCCTCAGTGCCCACTCTTCTGTGACAGCAAAAGATTAACACTCCAGTGAATTTAA 725
|||||
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Db 726 CGGGTTCATTTCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 785
QY 781 CCTGCTCTCATGCGCCACCGCGCTGGAGAGAGCGCCACCTGAGACAGTCCCGGACCG 840
Db 786 CCGTCTCTCATGCGCCACCGCGCTGGAGAGAGCGCCACCTGAGACAGTCCCGGACCG 845
QY 841 CCGAGCCCTGATACCAACAGTACCATACAGAGTGGCGAGACTTACGATCTCTGGCCCT 900
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QY 901 GGATACCACTACTGCTTCACTGCTCCACGGAGAGAACTGCTGGCGGACGCTTACAT 960
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QY 1261 CACCGGAGAGCG 1320
Db 1214 CACCGGAGAGCG 1273
QY 1321 TGCCCAAGCCCACTTGGGATGATTAAGCGCGCGCGCA 1359
Db 1274 TGCCCAAGCCCACTTGGGATGATTAAGCGCGCGCGCA 1311

RESULT 3
GGTFB1 1750 bp mRNA linear MAM 27-MAR-1996
LOCUS Porcine mRNA for transforming growth factor-beta 1.
DEFINITION X12373
ACCESSION X12373.1 GI:63808
VERSION 1
KEYWORDS transforming growth factor-beta 1.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 1750)
AUTHORS Jakowlew S.B.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-1988) Jakowlew S.B., National Institute of
health, National Cancer Institute, Laboratory of Chemoprevention,
Building 41, Room B902, Bethesda, Maryland 20892, USA
AUTHORS 2 (bases 1 to 1750)
TITLE Jakowlew S.B., Dillard P.J., Sporn M.B. and Roberts A.B.
Nucleotide sequence of chicken transforming growth factor-beta 1
(TGF-beta 1)
JOURNAL Nucleic Acids Res. 16 (17), 8730 (1988)
MEDLINE 88335639
PUBMED 3165520
COMMENT The submitters believe that the chicken cDNA library was
contaminated with porcine cDNA, and that the sequence is infect
porcine TGF-beta-1. 27-MAR-1996.
FEATURES
source Location/Qualifiers
1..1750 /organism="Sus scrofa"

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Best Local Similarity	94.8% Pred. No. 8,8e-208;											
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66	TAGTGTGACGCGCTGCG	125										
502	TAGTGTGACGCGCTGCG	561										
126	AGCTGTGACG	185										
562	AGCTGTGACG	621										
186	TTGCGAGCG	245										
622	TGCGCAGCG	681										
246	CTCTTTACACAGTACCG	305										
682	CTCTTTACACAGTACCG	741										
306	CAGAGCG	365										
742	CAGAGCG	801										
366	AAATCTATGATTAATTCGAAGGCGCACCCCGCACCTTATATATGCTGTTCGAACGCTCGG	425										
802	AAATCTATGATTAATTCGAAGGCGCACCCCGCACCTTATATATGCTGTTCGAACGCTCGG	861										
426	AGCTCCGGGAGCG	485										
862	AGCTCCGGGAGCG	921										
486	GCGTCAAGTTAAAGTGGAGCAGCAGTGAAGTATTCGAGAAATACGAAATGATGATTCCT	545										
922	GCGTCAAGTTAAAGTGGAGCAGCAGTGAAGTATTCGAGAAATACGAAATGATGATTCCT	981										
546	GCGGCTACCTCAGCAACCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	605										
982	GCGGCTACCTCAGCAACCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1041										
606	ATGTCAACCGGAGTTGTGCG	665										

Db	1042	ATGTCACCGGAGTGTGTGCGACAGTGGCTGAACCCGACAGAGGGCTATATGAGGTTTGTGCC	1101			
QY	666	TCAGTGGCCACTCTCTCTCTGACAGCAAAATATACACACTCTCACGTGTAATTAC---G	722			
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QY	723	GGTTCAATTCTGGCCGCGGGGGTACCTTGCCACCATTCACGGCATGACCGGCGCTTCC	782			
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QY	843	GAGCCCTGATATCAACACAGTACCCATACAGAGTGGCAGACTGAGATCTGTGCGCTGG	902			
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QY	963	ACTTCCGGAAGACACTGGGGCTGGAAGTGAATCATGAACCCAGGGCTACCATGCCAATT	1022			
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QY	1023	TCTGCTGGGGCCCTCTCTCCCTACATCTGAGACCTAGACACATCATGACAGCAAGTCTCTGG	1082			
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QY	1083	CTCTGTACAAACAGACACAACCCGGGGGGCGTGGGGGGCGCGTGTGCGTGGCGCAGAGCGC	1142			
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QY	1203	ACATATATCGTGGGTTCCCTGCAAGTGAAGTGAAGCCCGCCCGCCACACAGCCCGGCCCA	1262			
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QY	1263	CCGGCAGGCGCCGGGCCCAACCCCGCCCGCCCTACACCGGGGCTGTATTAAAGACATCGTG	1322			
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LOCUS	SSTGFBR	1605 bp	mRNA			
DEFINITION	Porcine mRNA for transforming growth factor-beta (TGF) precursor.		linear			
ACCESSION	Y00111					
VERSION	Y00111.1	GI:2129				
KEYWORDS	transforming growth factor-beta.					
SOURCE	Sus scrofa.					
ORGANISM	Sus scrofa					
REFERENCE	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.					
AUTHORS	Derynck,R. and Rhee,L.					
TITLE	Sequence of the porcine transforming growth factor-beta precursor					
JOURNAL	Nucleic Acids Res. 15 (7), 3187 (1987)					
MEDLINE	87174844					
PUBMED	3470708					
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Best Local Similarity 95.2%; Pred. No. 3.2e-191;
Matches 1176; Conservative 0; Mismatches 8; Indels 51; Gaps 1;
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RESULT 6
DOGTGFB1A
LOCUS
DEFINITION 1369 bp mRNA linear MAM 30-OCT-1994
cds
ACCESSION L34956
VERSION L34956.1 GI:516071
KEYWORDS homologue; transforming growth factor-beta 1;
SOURCE Canis familiaris adult jugular vein endothelial CDNA to mRNA.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 1369)
AUTHORS Manning, A.M., Auchampach, J.A., Drono, R.F. and Slightom, J.L.
TITLE Cloning of a canine CDNA homologous to human transforming growth
factor-beta 1 (TGFBeta1)
JOURNAL Unpublished (1994)
FEATURES
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Best Local Similarity 86.6%; Pred. No. 1,5e-169;
Matches 1148; Conservative 0; Mismatches 125; Indels 53; Gaps 3;

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Db 1321 CCAAGC 1326
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RESULT 7
E00973
LOCUS E00973 2527 bp RNA linear PAT 29-SEP-1997
DEFINITION E00973
ACCESSION E00973
VERSION E00973.1 GI:2169234
KEYWORDS JP 1986219395-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2527)
AUTHORS Riku,M.A.D.D. and Debitsudo,B.G.
TITLE NUCLEIC ACID CODED WITH TGF-BETA AND ITS USE
JOURNAL Patent: JP 1986219395-A 1 29-SEP-1986;
GENENTECH INC
COMMENT
OS human
PN JP 1986219395-A/1
PD 29-SEP-1986
PF 20-MAR-1986 JP 198606461
PR 22-MAR-1985 US 85 715142
PI RIKU MAIKERU ANDORE DERINKU, DEBITSDO BANNOOMAN GETSDERU PC
C12P21/00,C12N1/00,C12N5/00,C12N15/00/C12Q1/68,(C12P21/00, PC
C12R1:91),
PC (C12N1/00,C12R1:19),(C12N5/00,C12R1:91),(C12N15/00,C12R1:91);
CC strandedness: Double;
CC topology: Linear;
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BASE COUNT	472 a 888 c 735 g 432 t
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Query Match	72.0%: Score 979.6; DB 6; Length 2527;
Best Local Similarity	85.0%: Pred. No.1.4e-167;
Matches 1142; Conservative	0; Mismatches 149; Indels 53; Gaps 2;
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QY	126 AGCTGTGTAAACGGGAAGGCGCATCGAGGCATTTCCGGGCGACATTTGTGCCAAGCTGTGGC 185
Db	957 AGCTGTGTAAACGGGAAGGCGCATCGAGGCATTCGGGGCGCAAGTCTGTGCCAAGCTGTGGC 1016
QY	186 TTGCCAGACCCCCCGAGCCAGGGGGAGCTGTCGCCGCCGCCGCTGCTGTAGAGCGTACTGG 245
Db	1017 TTGCCAGACCCCCCGAGCCAGGGGGAGGTTGTCGCCGCCGCCGCTGCTGTAGAGCGTACTGG 1076
QY	246 CTCCTTTACACAGTATCCCGCGCGCGGGTATGGCGGGGAAGTGTGCACCGCGGACCGCGAGC 305
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QY	366 AAATCTATGATTAATTTCAAGGGCACCCCCCAAGCTTATATATGCTGTGTCAACAGCTGGG 425
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QY	426 AGCTCCGGGAAGCGGTGCCGGAACTGTATTGCTCTCTCGGGCAGAGGCTGCGCTGTGTA 485
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QY	546 GAGCGTACTACAGCAACCGGCTGCTGGGCCCCCAAGTACACCGGAGTGGCGTCTTTTG 605
Db	1377 GAGCGTACTACAGCAACCGGCTGCTGGGCAACCCAGGACTCTGCGCAGATGTGTTATCTTTTG 1436
QY	606 ATGTACCCGGAGTGTGCGGAGTGGCTGACCCCGCAGAGAGGCTATTAGAGGGTTTTTCGC 665
Db	1437 ATGTACCCGGAGTGTGCGGAGTGTGAGCCCGGAGGGGAATATGAGGCGCTTTTCGC 1496
QY	666 TCAGTGGCCACTCTTCCCTCTGACAGCAAAAGTATACACTCTCCAGTGGAAATATACGGGT 725
Db	1497 TTAGGCGCCACTGCTCTCTGTATACACAGGATTAACACTGTCAATGTGACATCAACAGGGGT 1556
QY	726 TCAATTTGCGCGCGCGGGGTGACCTGGGCGCACATTTCAAGGATGAACCGGCGCTTCTGC 785
Db	1557 TCACATACCGGCGCGCGGAGTGAACCTGGGCGCACATTTCAATGAGCATGAACCGGCGCTTCTGC 1616
QY	786 TCTCTATGCGCACCCCGCTGGAAGGGGCCACACCTGTACACAGCTTCCGGGACCGCGGAG 845
Db	1617 TTTCTATGCGCACCCCGCTGGAAGGGGCCACACATCTCAAAAGCTTCCGGGACCGCGCA - 1675
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QY	186	TTGGCCAGCCCCCGGAGCCAGAGGGGAGTGTGGCCGCCGCCGCTGTCCAGGACACTACTGG	245
Db	1017	TGGCCAGCCCCCGGAGCCAGAGGGGAGTGTGGCCGCCGCCGCTGTCCAGGAGCCGTGTCC	1076
QY	246	CTCTTTACAACAAGTACCCGCGAGCCGGGTAGCCGGGAAAGTGTGCAACCGAGGCCGAGC	305
Db	1077	CCCTGTACAACAGCACCCCGAGCCGGGTAGCCGGGAGAGTGTGCAACCGAGGCCGAGC	1136
QY	306	CAGAGGGGAGACTACTACGCCAGAGAGTCAACCCCGCTGCTAATGTGTGAACGCGCAAC	365
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QY	366	AAATCTATGATTAATTAACAAGGGAGACCCCGACAGCTTATATATGTCTTCAACAACGTGG	425
Db	1197	AAATCTATGATTAATTAACAAGGGAGACCCCGACAGCTTATATATGTCTTCAACAACGTGG	1256
QY	426	AGCTCCGGGAGCGGTGCGGGAACCTGTATTGTCTCTCGCGGAGAGCTCGCGCTGCTGA	485
Db	1257	AGCTCCGGAAGACGGTACTGTAAACCGGTGTGTCTCTCGCGGAGAGCTCGCGTGTCTGA	1316
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QY	606	ATGTACCGGAGTGTGCGGCAAGTGGCTGACCCGAGAGAGGCTATAGAGGTTTTCGCC	665
Db	1437	ATGTACCGGAGTGTGCGGCAAGTGGCTGACCCGCTGAGAGGGAATTAGAGGCTTTCGCC	1496
QY	666	TCAGTGGCCACCTCTTCTCTGACAGCAAGATTAACACACTCCACGTGTGAATTAACGGGT	725
Db	1497	TTAGGCGCCACCTGTCTCTGTGACAGAGGATTAACACACTGTCAAGTGTGACATCAACGGGT	1556
QY	726	TCAATTTCTGGCCGGGGGTGACCTGGCCACATTACGGCATGAACCGGCCCTCTCTGC	785
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QY	786	TCCTCATGCGCACCCCGCTGGAGAGGGCCAGACCTTGACAGCTCCCGGACACGGCCGAG	845
Db	1617	TTCTCATGCGCACCCCGCTGGAGAGGGCCAGATCTGCAAAAGCTCCCGGACACGGCCGA	1675
QY	846	CCCTGGATTACCAACAGCTACCCATACAGAGCTGCGAGACTACGCACTCTGGCCCTGGATA	905
Db	1676	-----GCCCTGGACA	1685
QY	906	CCAATCTAGCTTCAAGCTCACGAGAAAGACGTGCGGTGGGGAGCTCTACATGAGCT	965
Db	1686	CCAATCTATTTGCTTCAAGCTCACGAGAAAGACGTGCGGTGGGGAGCTTACATTTGACT	1745
QY	966	TCGGAAGAGACCTGGGCTGGAAGTGGATTATGAACCCCAAGGGCTACCATGCAATTTCT	1025
Db	1746	TCGGAAGAGACCTGGGCTGGAAGTGGATTATGAACCCCAAGGGCTACCATGCAACTTCT	1805
QY	1026	GCCTGGGGCCCTGTCCCTCACTCTGGAGCCTTGACACTCAAGTACAGCAAGTCTGTGGCTC	1085
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QY	1086	TGTACACACAGACAACCGGGCGGTGGGGCGCGCGGTGCGGTGCGGCAAGGCGCTGG	1145
Db	1866	TGTACACACAGCATAACCGGGCGCTTGGGCGCGCGGTGCGGTGCGGCAAGGCGCTGG	1925
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Db	2046	GCCGCGCCCAACCCCGCCCGCCCGCTGCCCTTCGCCCATGGGAGCTGTATTAAAGACA	2105					
OY	1318	TGCTGCCCAAGCCCACTTTGGGATCGATTAAA	1349					
Db	2106	CCGTGCCCAAGCCCACTGGGAGCCGCCATTAA	2137					
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LOCUS	OATGFBI							
DEFINITION	O.aries mRNA for transforming growth factor-beta I.	1173 bp	mRNA	linear	MAM 18-Apr-1995			
VERSION	X76916							
KEYWORDS	X76916.1 GI:496648							
SOURCE	TGF-beta 1; transforming growth factor-beta 1.							
ORGANISM	Ovis aries							
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;							
	Bovidae; Caprine; Ovis.							
REFERENCE	1 (bases 1 to 1173)							
AUTHORS	Woodall,C.J., McLaren,L.J. and Watt,N.J.							
TITLE	Sequence and chromosomal localisation of the gene encoding ovine latent transforming growth factor-beta 1							
JOURNAL	Gene 150 (2), 371-373 (1994)							
MEDLINE	95121932							
PUBMED	7821809							
REFERENCE	2 (bases 1 to 1173)							
TITLE	Woodall,C.							
JOURNAL	Direct Submission							
	Submitted (24-DEC-1993) C. Woodall, Univ. of Edinburgh, Dept. of Veterinary Pathology, Sc. of Vet. Studies, Univ. of Edinburgh, Edinburgh EH9 1QH, UK							
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Matches 1086; Conservative	0; Mismatches 87; Indels 51; Gaps 1;							
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OY	131	GTGAAGCGGAAGCCCATTCAGAGCCATTGCGGCGAGATTCCTGTCGAAGCTTCGAGCTTGGC	190					

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LOCUS
DEFINITION
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MGC:3119 IMAGE:3351664, mRNA, complete cds.
ACCESSION
BC000125
VERSION
BC000125.1 GI:12652748
KEYWORDS
MGC.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1780)
REFERENCE
Strausberg, R.
Direct Submission
Submitted (03-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
Info@cgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chin, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schell, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stolt,
Michael Thorne, Miranada Tsai, Natasha van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAL Plate: 6 Row: e Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency OR
analysis.
FEATURES
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BASE COUNT
341 a 648 c 493 g 298 t
ORIGIN
Query Match 71.4%; Score 972.4; DB 9; Length 1780;
Best Local Similarity 84.5%; Pred. No. 2,9e-166;
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Qy	66	TAGTGTGACACCTCTGGCGCGCGCGCCGCGACTGTCCACCTGCAAGACCATGCACATGG	125
Db	502	TGGTGTGACGCTCTGGCGCGCGCGCGGACTATCCACCTGCAAGACCATGCACATGG	561
Qy	126	AGCTGTGTAAACGGGAAGCGCATCCAGGGCATTTCCGGGCCAAGTTCTGTCCAAAGCTTCGGCG	185
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Qy	666	TCAGTGTCCCACTTCTCTCTGTGACAGCAAAAGATTAACACACTCCACGTGTGAATTAACGGGT	725
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Qy	726	TCAAATCTGTGGCGCGCGGGGTGACTGGCACCAATTCACGGGATGAAACCGGCGCTTCTGTGC	785
Db	1162	TCACTACCGGGCGCGCGAGGTGACTGGCACATTTCAATGSCATGAAACCGGCGCTTCTGTGC	1221
Qy	786	TCCTATGTGGCCACCCGCTGTGAGAGGAGGCCAGCACTGCACAGCTCCGGCACCGCGCGAG	845
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Qy	1026	GGCTGGGGCCCTGTCCCTATCATCTGTGAGGCTTAGACATCTAGTACAGAAAGTCTCTGGCTC	1085
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Db	1651	GCGCGCGCCACCGCGCGCGCGCGCGCGCTGCTGCCATGGGGGCTGTATTTAAGACA	1710
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VERSION	BC001180.1 GI:12654682
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SOURCE	Homo sapiens.
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REFERENCE	
AUTHORS	
TITLE	
JOURNAL	

REMARK	COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov	Contact: MGC help desk

Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosset, Yaron Buterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reia Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carlie Mathewson, Candice Mcleavy, Steven Ness, Pawan Pandoh, Anna-Liisa Piribuu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stolt, Michael Thorne, Miranada Tasi, Natasya van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMW at: <http://image.llnl.gov>
Series: IRAL Plate: 6 Row: e Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 37097.

FEATURES	Location/Qualifiers
source	1. .1780

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/db_xref="taxon:9606"
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/lab_host="DH10B-R"
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AA7 1619
CDS

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CDS
447..1015
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LSAHCSDSDNDLTQVDINGFTTGRGLATIHGMNRPFLMLAPLEAHOHLSRHR
RRALDNYCRSSSTERKNCVRLYIDFRKDLGMKWHHEPKGYHANCLEGPYIWSIDT
QYSKVLATYMNQHNNGASAPAPCCVPALEPLRIVYVGRKPKVEQLSNMIVRSCKCS"
BASE COUNT      341 a      648 c      493 g      298 t
ORIGIN

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Query Match      71.4%; Score 972.4; DB 9; Length 1780;
Best Local Similarity 84.5%; Pred. No. 2.9e-166;
Matches 1142; Conservative 0; Mismatches 151; Indels 59; Gaps 2;

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QY      6  CCGAGATGGGCGCTTGGGGCTTGGGCTCTTGGCCGTGCTGCTGCCGCGTGTGCTGC
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QY      66  TAGTGTGACGCTGGCGCGCGCGCGCGCGCGACTGTCACCTGCAAGACCATGACATGG
DB      502  TGGTGTGAGAGCCCTGGCGCGCGCGCGCGCGCGACTGTCACCTGCAAGACTATGACATGG
QY      126  AGCTGTGAAGCGGAGCGCGATCGAGGCGCATTCGGGCGCATTCGTCAGAGCTTCGGC
DB      562  AGCTGTGAAGCGGAGCGCGATCGAGGCGCATTCGGGCGCGCATTCGTCAGAGCTTCGGC
QY      186  TTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
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QY      246  CTCCTTACACAGTACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
DB      682  CCTGTACACAGTACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY      306  CAGAGCGGAGTACAGGAGAGTACAGGAGTACAGGAGTACAGGAGTACAGGAGTAC
DB      742  CTGAGGCGCGCTACTACGCGCAAGGAGGTCACCGCGCTGCTATGTTGGAACCCAC
QY      366  AATATCTATGTAATTCACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
DB      802  AATATCTATGTAATTCACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY      426  AGCTCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
DB      862  AGCTCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY      486  GCGTCAAGTTAAAGTGAGCAGCAGTGAAGTATACAGAAATACAGCAATTTGCT
DB      922  GCGTCAAGTTAAAGTGAGCAGCAGTGAAGTATACAGAAATACAGCAATTTGCT
QY      546  GCGGCTACCTCAGCAACCGGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG
DB      982  GCGGCTACCTCAGCAACCGGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY      606  AATGTCACGAGTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
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DB      1102  TTAAGCGCCCACTCTCTCTCTGACAGCAAAAGATAACACACTCAGCTGGAATTAACGG
QY      726  TCAATTTCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
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QY      786  TCCCTATGCGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
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QY      846  CCTGTATACAAACAGCTACCCATACGAGTGGCAGACTACGATCTCTGGCCCTGATTA
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QY      966  TCCGAGAGACCTGGGCTGGAAGTATTCATGACCCAAAGGCTACCATGCAATTTCT
DB      1351  TCCGAGAGACCTGGGCTGGAAGTATTCATGACCCAAAGGCTACCATGCAATTTCT
QY      1026  GCGTGGGCGCGCTGCTCCCTCATCTGAGCGCTGACACTGATACAGCAAGTCTGCTC
DB      1411  GCGTGGGCGCGCTGCTCCCTCATCTGAGCGCTGACACTGATACAGCAAGTCTGCTC
QY      1086  TGTACACAGCAACCCGGGCGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG
DB      1471  TGTACACAGCAATTAACCGGCGCGCTGCGGCGCGCGCGCGCGCGCGCGCGCG
QY      1146  AGCCACTGCGCGCTGCTCCCTCATCTGAGCGCTGACACTGATACAGCAAGTCTGCTC
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QY      1206  TGATGTCGCTTCTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT
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QY      1318  TCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
DB      1711  CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG

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RESULT 12

AGMTGFB

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

FEATURES

source

CDS

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1. 1561
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KLAEVQHELVEYOKYSNNSWRYLSNRRLAPSPSEWLSFDVGVVPMQLSRGEIEGFR
LSAHCSDSDNDLTQVDINGFTTGRGLATIHGMNRPFLMLAPLEAHOHLSRHR
RRALDNYCRSSSTERKNCVRLYIDFRKDLGMKWHHEPKGYHANCLEGPYIWSIDT

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FEATURES	source
LOCUS	BC022242
DEFINITION	Homo sapiens, clone MGC:22008 IMAGE:439762, mRNA, complete cds.
ACCESSION	BC022242
VERSION	BC022242.1 GI:18490115
KEYWORDS	MGC.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 1746)
TITLE	Strausberg, R.
JOURNAL	Direct Submission Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT	Contact: MGC help desk Email: cgabps-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcdepaxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAP Plate: 27 Row: e Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

Location/Qualifiers
1..1746

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Comugen Ltd.

OW nucleic - nucleic search, using sw model

Run on: April 15, 2003, 10:00:25 ; Search time 362 Seconds

(without alignments)
8466.767 Million cell updates/sec

Title: US-10-017-372e-36

Perfect score: 1361

Sequence: 1 tggatccagatagcggcctt.....cgattaagcgccgagact 1361

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1211.8	89.0	1326	24	AAD22696
2	978.8	71.9	2537	7	AAN60972
3	978.8	71.9	2537	11	AAO03301
4	978.8	71.9	2537	11	AAO02814
5	978.8	71.9	2537	17	AAT15720
6	977.2	71.6	2537	15	AAO56923
7	974	71.3	2537	19	AAV52933
8	971	71.3	1561	11	AAO03268
9	969.4	71.2	2742	22	AAI58342

10	968.6	71.2	1559	13	AAO20289
11	968.2	71.1	1821	12	AAO13392
12	967.6	71.1	1560	9	AAN81084
13	967.6	71.1	1560	11	AAO03508
14	965.8	71.0	2745	16	AAT05876
15	965.8	71.0	2745	22	AAH28216
16	957.8	70.4	1303	13	AAO09317
17	956.8	70.3	1405	15	AAO55624
18	954.8	70.2	1571	11	AAO03269
19	949.8	69.8	1569	9	AAN81085
20	946.6	69.6	1569	11	AAO03509
21	940.6	69.1	1561	11	AAO04908
22	937.4	68.9	1561	13	AAO29177
23	916.6	67.3	1176	24	ABL91703
24	896	65.8	1565	13	AAO29178
25	797.4	58.6	2765	22	AAT160128
26	776.2	57.0	2208	13	AAO20291
27	774.6	56.9	2206	11	AAO03510
28	774.6	56.9	2207	11	AAO03511
29	773	56.8	2207	11	AAO05127
30	761.6	56.0	2217	10	AAN90768
31	755.4	55.5	2200	16	AAT04115
32	684.6	50.3	2773	23	AA584421
33	678.8	49.9	834	12	AAO12192
34	522.6	38.4	875	23	AA570979
35	357.6	26.3	650	24	ABK84023
36	357.6	26.3	650	24	ABL68818
37	354.4	26.0	489	24	ABL99528
38	310.2	22.8	339	18	AAT42771
39	310.2	22.8	339	20	AAV99375
40	308.6	22.7	339	17	AAT17235
41	308.6	22.7	339	20	AAI15245
42	308.6	22.7	3541	17	AAT16516
43	308.6	22.7	3541	21	AAI12498
44	307	22.6	339	12	AAO11993
45	307	22.6	339	17	AAT15462

ALIGNMENTS

RESULT 1	
AAD22696	
ID	AAD22696 standard; cDNA; 1326 BP.
AC	
XX	AAD22696;
DE	26-FEB-2002 (first entry)
XX	
DE	Porcine transforming growth factor beta 1 (TGF-beta1) cDNA.
XX	
KW	Porcine; transforming growth factor beta 1; TGF-beta1; gene therapy;
KW	IBD; inflammatory bowel disease; autoimmune disease; immunosuppressive;
KW	multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW	diabetes mellitus; sarcoidosis; psoriasis; dermatological; ss.
XX	
OS	Sus scrofa.
XX	
FT	Key
FT	Location/Qualifiers
FT	16..1188
FT	/*tag- a
FT	/product= "Porcine TGF-beta1 mutant protein"
XX	
XX	WO200181404-A2.
XX	
XX	01-NOV-2001.
PD	
XX	20-APR-2001; 2001WO-US12980.
PF	
XX	Sequence of pre-TG
XX	Pre-transforming g
PR	Human pre-TGF-beta
XX	Human pre-transfor
XX	Simian transformin
PA	
XX	Human polynucleoti
XX	
XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.

Sequence encoding
Human pro-TGF-beta
Coding sequence of
Simian Transformin
cDNA encoding tran
Nucleotide sequenc
Monkey transformin
TGFbeta1 5'-UTR-CD
Human transforming
Coding sequence of
Human Transforming
Sequence encoding
TGF-beta 1/beta 2
Human polynucleoti
TGF-beta1. Homo
Human polynucleoti
Sequence encoding
Human Transforming
Hybrid transformin
Human TGF-beta1/TG
Sequence of human
Simian-human hybr
DNA encoding novel
Sequence encoding
DNA encoding novel
Human cDNA diffe
Kidney cancer rela
Target canine gene
TGF-beta1 active f
cDNA encoding a tr
Human TGF-beta 1 c
cDNA encoding the
Collagen AI/TGF-be
cDNA encoding a ch
Transforming Growt
Human transforming

PI Strober W, Nakamura K, Kitani A, Fuss IJ;

XX WPI; 2002-026155/03.

DR P-PSDB; AAEI3596.

XX Composition for treating autoimmune diseases e.g. inflammatory bowel
PT disease in humans, comprises vector containing transforming growth
factor-beta under the control of inducible promoter

XX Claim 1; Fig 1; 78pp; English.

CC The invention relates to a composition containing a vector comprising a
CC gene encoding a regulatory transcription factor under the control of a
CC promoter encoding a transforming growth factor-beta (TGF-beta). The
CC vector is useful for expressing TGF-beta, such as TGF-beta1, TGF-beta2
CC or TGF-beta3, its variants or homologues, by transfecting a cell which
CC is part of a host suspected of having an autoimmune disease, especially
CC inflammatory bowel disease (IBD), under conditions such that the
CC polypeptide encoded by the nucleic acid sequence in the vector is
CC expressed. The vector is delivered using a delivery system. The delivery
CC of the vector results in substantial elimination of symptoms of the
CC autoimmune disease and increased production of IL-10 by the host. The
CC composition is useful for treating various diseases with an autoimmune
CC component such as multiple sclerosis, rheumatoid arthritis, systemic
CC lupus erythematosus, insulin-dependent diabetes mellitus, sarcoidosis
CC and psoriasis, and also for assaying the expression of a gene in a cell.
CC The vector is further useful for screening of the effect of test
CC compounds on cytokine (e.g. TGF-beta) expression of transfected cells.
CC The present sequence is a cDNA encoding porcine TGF-beta1 mutant.

XX Sequence 1326 BP; 263 A; 438 C; 392 G; 233 T; 0 other;

Query Match 89.08; Score 1211.8; DB 24; Length 1326;

Best Local Similarity 95.68; Pred. No. 5.4e-233;

Matches 1299; Conservative 0; Mismatches 7; Indels 53; Gaps 3;

QY 1 TGGTACCGAGATGAGCGCTTGGGGCTCGGCTTGGCGTGTGCTGCGCTGCGTGGTG 60
DB 6 TGGTACCGAGATGAGCGCTTGGGGCTCGGCTTGGCGTGTGCTGCGCTGCGTGGTG 65
QY 61 GCTGCTAGTGTGAGCGCTTGGCGCGCGCGCGGCTGTGCTGCTGCTGCTGCTGCTG 120
DB 66 GCTGCTAGTGTGAGCGCTTGGCGCGCGCGCGGCTGTGCTGCTGCTGCTGCTGCTG 125
QY 121 CATGAGCTGTGTGAGGGGAGCGCATGAGCGCATTGGCGCGCATTTCTGTCCAACT 180
DB 126 CATGAGCTGTGTGAGGGGAGCGCATGAGCGCATTGGCGCGCATTTCTGTCCAACT 185
QY 181 TCGGCTTGGCGAGCG 240
DB 186 TCGGCTTGGCGAGCG 245
QY 241 ACTGCGCTTTTACACAGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 246 ACTGCGCTTTTACACAGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 305
QY 301 CGAGCCGAGGCGGAGTACTAGCGCAAGGAGGTACCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 306 CGAGCCGAGGCGGAGTACTAGCGCAAGGAGGTACCGCGCGCGCGCGCGCGCGCGCGCG 365
QY 361 CAACCAATCTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
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QY 421 GTGGAGCTCCGGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
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DB 486 GCTGAGGCTCAAGTAAAGTGAAGGAGCAGCAGTGGAGGTATACCAAGTAATACAGCAATGA 545
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QY 601 CTTTATGTACCGGAGGTGTGGCGAGTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 606 CTTTATGTACCGGAGGTGTGGCGAGTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 665
QY 661 TCGCCTCACTGCG 720
DB 666 TCGCCTCACTGCG 725
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DB 726 CGGCTTCAATTTGTGCG 785
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DB 786 CTTGCTTCCATGCG 845
QY 841 CCGAGCCCTGGATACCAAGCTTACCGATAGCAGTGTGCGCGCGCGCGCGCGCGCGCGCT 900
DB 846 CCGA-----GCCCT 854
QY 901 GGATACCAACTACTGCTTACGCTCCACGAGAGAACTGCTGCTGCGCGCGCGCGCGCGCG 960
DB 855 GGATACCAACTACTGCTTACGCTCCACGAGAGAACTGCTGCTGCGCGCGCGCGCGCGCG 914
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DB 915 TGACTTCCGGAAGACCTTGGGCTGGAAGTGTATGATGACCAAGGCTTACATGCGCA 974
QY 1021 TTTTTCGCTGGGCG 1080
DB 975 TTTTTCGCTGGGCG 1034
QY 1081 GGCCTGTATCAACACGACCAACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
DB 1035 GGCCTGTATCAACACGACCAACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1094
QY 1141 GCTGAGGCGACG 1200
DB 1095 GCTGAGGCGACG 1154
QY 1201 CAACATGATCTGCG 1260
DB 1155 CAACATGATCTGCG 1213
QY 1261 CACCGGCGAGGCG 1320
DB 1214 CACCGGCGAGGCG 1273
QY 1321 TGCCCAAGCCACTTGGGATGATTAAAGCGCGCGCG 1359
DB 1274 TGCCCAAGCCACTTGGGATGATTAAAGGTTGAGAGA 1311

RESULT 2
AAN60972
ID AAN60972 standard; cDNA; 2537 BP.
XX
XX AAN60972;
AC
XX
XX 28-Oct-1991 (first entry)
DE
XX Sequence encoding preTGF-beta.
XX
XX Transforming growth factor beta; cancer; wound healing.
KW
XX
XX Key Location/Qualifiers
FT misc-structure 37..113
FT /note= "a
FT /note= "Sequence can form stable hairpin loops"
FT CDS 842..2014

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FT      mat_peptide      /*tag= b
FT      1676, 2011
FT      /*tag= c
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XX      EP200341-A.
XX
XX      10-DEC-1986.
XX
XX      21-MAR-1986;      86EP-0302112.
XX      PF
XX      PR      22-MAR-1985;      85US-0715142.
XX      PR      13-MAR-1987;      87US-0025423.
XX      PA
XX      (GETH ) GENENTECH INC.
XX
XX      Derynck RMA;
XX      PI
XX
XX      WPI; 1986-326875/50.
XX      DR
XX      P-PSDB; AAP61468.
XX
XX      TGF-beta prodn. from transformed hosts - useful esp. for treating
XX      PT      wounds (J6 2/9/86).
XX      ST
XX
XX      Disclosure; Fig 1b; 26pp; English.
XX      PS
XX
XX      The gene product is known to stimulate cell proliferation and
XX      CC      inhibit anchorage-dependent growth of a variety of human cancer cell
XX      CC      lines, it is esp. useful in treatment of burns and the promotion of
XX      CC      surface and internal wound healing. TGF-beta may be expressed from a
XX      CC      transformed CHO cell line.
XX
XX      Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;

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Query Match	71.9%	Score 978.8	DB 7	Length 2537
Best Local Similarity	84.8%	Pred. No. 5e-188		
Matches 1146; Conservative	0	Mismatches 147	Indels 59	Gaps 2

OY	6	CGAAGTGGCGCCTTGGGGAGCTGGGGCTGTGGCGGTGCTGCCCTGTGGCTGTGGCTGC	65
Db	837	CCCCATGGCGCCCTCGGGGCTGGGCTGTGGCGGTGCTGCCCTGTGGCTGTGGCTGC	896
OY	66	TAGTGTGACGCGCTGGCGCGGCGCGCGGAGCTGTGCACCTGGAAACCATGCACATGG	125
Db	897	TGGTGTGACGCGCTGGCGCGGCGCGCGGAGCTATTCACCTGCAGACATGTGCACATGG	956
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Db	957	AGCTGGTGAAGCGGAAGCCGATCGAGGCCATCCGCGGCGCAGATCTGTCCAAAGCTTGCG	1016
OY	186	TTCGCCAGCCCCCGAGCCAGAGGGGAGACTGTGCGCCCGCGCGCTGCTTGAGGCACTACTGG	245
Db	1017	TTCGCCAGCCCCCGAGCCAGAGGGGAGGTGCGCCCGCGCGCTGCTGCCAGGCGCTGCTCG	1076
OY	246	CTCTTTACAACAGTACC CGCGAGCCGGGTTGGCGGGGGAAGTGTGCAACCGGAGCGCCGAGC	305
Db	1077	CCCTGTACAACAGCACCCCGCGAGCCGGGTTGGCGGGGGAAGTGTGCAAGAACCGGAGCGCAGC	1136
OY	306	CAGAGCGGAGTACTACTACGGCCAAAGGAGGTCAACCGCGGTGTAATGTGTGAAAGCGGCAC	365
Db	1137	CTGAGGCGGACACTACTACGCCCAAGGAGGTCAACCGCGGTGTAATGTGTGAAAGCCACACAG	1196
OY	366	AAATCTATGATAAATTCAAGGGGCACCCCACAGCTTATATATGCTGTTCAACACGTCGG	425
Db	1197	AAATCTATGATAAAGTTCAAGGAGAGATACACAGACAGCATATATATGTTCTTCAACACATCAG	1256
OY	426	AGCTCGGGAAGCGGTGCGCGGAACCTGTATTTCTCTCTGGGCGAGACTGGCGCTGCTGA	485
Db	1257	AGCTCGGAAGGCGGTACTGTGAACCCCTGTTCTCTCCCGGAGAGACTCGTCTGCTGA	1316
OY	486	GGCTCAAGTTAAAAGTGGAGACACAGTGGAGGTATACCGAANAATACAGCATATATCTCT	545
Db	1317	GGCTCAAGTTAAAAGTGGAGACACAGCTGGAGGTATACCGAANAATACAGCAACATTTCTT	1376

QY	546	GGGCTACTCTAGCAACCGGGCTGTGGCCCCCAGTACTACCGGAGTGGCTGTCTTTG	605
Db	1377	GGCGATCTCTAGCAACCGGGCTGTGGCCCCCAGTACTACCGGAGTGGCTGTCTTTG	1436
QY	606	ATGTACCGGAGTGTGGCGGAGTGGCTGTGGCCCCGAGAGAGGCTATAGAGGTTTGGCC	665
Db	1437	ATGTACCGGAGTGTGGCGGAGTGGCTGTGGCCCCGAGAGTGGCTATAGAGGTTTGGCC	1496
QY	666	TCAGTCCCACTCTCTCTGTACAGCAAGATTAACAACACTCCACGTGGAAATTAACGGGT	725
Db	1497	TTTAGCGCCCACTCTCTCTGTACAGCAAGGATTAACAACACTCCAGTGGACATCAACGGGT	1556
QY	726	TCATTTTGGCGCGGGGGTGAACCTTGGCAACATTCACGGGCAATGAACCGGCCCTTCTGCG	785
Db	1557	TCATTAACGGCGCGGGGGTGAACCTTGGCAACATTCATGAGCAATGAACCGGCCCTTCTGCG	1616
QY	786	TCCTATGCGCCACCCGCGTGGAGAGGGGCCAGCACTGTGCACAGCTCCGGCACCGCGAG	845
Db	1617	TTTCATGCGCCACCCGCGTGGAGAGGGGCCAGCATGTGTGAACAGCTCCGGCACCGCGGA	1675
QY	846	CCCTGGATACCAACAGCTACCCATACAGAGTGGCCAGACTATCTGTGGCCCTGGATA	905
Db	1676	-----GCCCTGGACA	1685
QY	906	CCAACTACTGCTTACAGCTCCACAGGAGAGAACTGCTGCGTGGGCGAGCTTCTACTTTGACT	965
Db	1686	CCAACTATTGCTTTCAGCTCCACAGGAGAGAACTGCTGCGTGGGCGAGCTTCTACTTTGACT	1745
QY	966	TCGCGAAGAGCACTGGGCTGGAAAGTGGATTCTATGAACCCCAAGGGCTTACATGCCAATTCT	10255
Db	1746	TCGCGAAGAGCACTGGGCTGGAAAGTGGATTCTACACAGGCCCAAGGGCTTACATGCCAATTCT	18055
QY	1026	GGCTGGGGGCGCTGTCCCTACATCTGGAGCTTAACACTCTAGTAACAGAAAGTCTTGCTC	10855
Db	1806	GGCTGGGGGCGCTGTCCCTACATTTTGAAGCTTGACACAGCATAGCAAGAGTCTTGCTC	18655
QY	1086	TGTACACACAGTACAAACCCGGGGCGCTTCGCGGGCGGCTGCTACGTGCCAGGCGCTGG	11455
Db	1866	TGTACACACAGTAAACCCGGGGCGCTTCGCGGGCGGCTGCTACGTGCCAGGCGCTGG	19255
QY	1146	AGCCACTGCGCCATCGTGTACTACGTGTGGCGCGCAAGCCCAAGGTGGAGCACTGTCCACA	12055
Db	1926	AGCCCTCTGCCATCGTGTACTACGTGTGGCGCGCAAGCCCAAGGTGGAGCACTGTCCACA	19855
QY	1206	TGATGTGGGCTTCTGTACAGTGTGAGGCCCGCGCCGCCACACAGCCCGCGCCACCC	12855
Db	1986	TGATGTGGGCTTCTGTACAGTGTGAGGTTCGGCCCCCGCCCGCGCCCGCGGAG	20455
QY	1266	GGCAGGCCCGGCCACCCCGCGCGCT-----CACCGGGGCTGTATTAAAGACA	1317
Db	2046	GGCCGCGCCACCCCGCGCGCGCGCTGTGCGCATGGGGGCTGTATTAAAGACA	21055
QY	1318	TCGTGCCCCAAGCCCACTTGGGATGCATTAA	1349
Db	2106	CCGTGCCCCAAGCCCACTTGGGATGCATTAA	2137

RESULT 3	
AAQ03301	
ID	AAQ03301 standard; DNA; 2537 BP.
XX	
AC	AAQ03301;
XX	
DT	05-AUG-1990 (first entry)
XX	
DE	cdna encoding human pre-transforming growth factor-beta-1 (pre-TGF-beta-1).
DE	
XX	
KW	Transforming growth factor-beta-1 (TGF-beta-1);
KW	neoplastic cell line inhibition;
KW	EGF-potentiased anchorage-independent growth;
XX	
OS	Homo sapiens.

[illegible]

QY	126	AGCTGCTGTAACGGAGAGCGCATTCAGAGCCATTTCGGGGCACAATTCTGTGCAAGCTTGCGGC	185
Db	957	AGCTGCTGAACCGGAAGGCGATTCAGAGGCTATCCGGGCGAAGTCTGTGCACAGCTGCGGCG	1016
QY	186	TTGCGAGGCCCCCGAGCGCAGAGGGAGCATGTGCCGCCCGCCCGCTGCTGACTGAGGCACTACTGG	245
Db	1017	TCGGCAGGCCCCCGAGGCCAGGGGGAGGTTGCCGCCCGCCGCTGCTGCCAGGCGCTGTCTCG	1076
QY	246	CTCTTTACACAAGTACCCGCCGACCGGGTAAAGCCGGGGAAAGTGTCCAAACCGGAGCCCGAGC	305
Db	1077	CCCTGTACACAAGCACCCCGCGACCGGGTGGCGGGGAGAGTGCACAAACCGGAGCCCGAGC	1136
QY	306	CAGAGCGGAGCTACTACGCGCAAGGAGGATCACCCGGGTGCTAATGGTGGAAACCGGCAAC	365
Db	1137	CTGAGGCGGAGCTACTACGCGCAAGGAGGATCACCCGGGTGCTAATGGTGGAAACCCCAACAAG	1196
QY	366	AAATCTATGATTAATTTCAAGGGGACCCCGCCACAGCTTATATGTCTTTCAACACGTCGG	425
Db	1197	AAATCTATGATTAATTTCAAGCGAGCTATACACAGCATATATATGTCTTTCAACACATCAG	1256
QY	426	AGCTCCGGGAACGGGTGGCGGGAACCGTATTCCTCTCTCGGGCAGAGCTGCGCTGTCTGA	485
Db	1257	AGCTCCGGAAGACGGTACTGATGAACCCGTCTTGTCTCTCCGGCAGAGCTGCGCTGTCTGA	1316
QY	486	GGCTCAAGTTAAAGTGGAGCAGCACTGGAGCTATATCCAGAAATACAGCAATGATTCT	545
Db	1317	GGCTCAAGTTAAAGTGGAGCAGCACTGAGCTGTACAGAAATACAGCAATATCTCT	1376
QY	546	GGCGCTACTCTGACAGCAACCGGCTGTGCGCCCGCAGTATACACCGGAGGCTGCTCTTG	605
Db	1377	GGCGATATCTCGACAAACCGGCTGTGCGCACCCAGCGACTGTGGCAGTGTATATCTTTTG	1436
QY	606	ATGTCAACCGAGATTGTGGCGGAGTGGCTATACCCGCGAGAAGGCTATAGAGGATTTTCGCC	665
Db	1437	ATGTCAACCGGAGATTGTGGCGGAGTGTATACCGGTGAGGGGAAATTGAGGGCTTTTCGCC	1496
QY	666	TCAGTCCCACTTCCTCTGTACAGCAAAAGATTACCACTCCACGTGGAAATTAACGGGT	725
Db	1497	TTAGCCGCCCACTGCTCTCTGTACAGCAGGAGATTACACTGTCAAGGTGAGCATCAACGGGT	1556
QY	726	TCGAATCTGGCGCGGGGGTGAAGCTGGCCACACATTCACGGCATGAACCGGCTTCCTGCG	785
Db	1557	TCACTACCGGCGCGGAGGTGACTGTGGCCACATTCATGATGATGAACCGGCTTCCTGCG	1616
QY	786	TCCTCATGGCCACCGCGTGGAGAGGGCCACGACCTGCACAGCTCCCGGACCCCGGAG	845
Db	1617	TTCTCATGGCCACCGCGTGGAGAGGGCCACGATTCGTGCMAAAGCTCCCGGACCCCGCGA	1675
QY	846	CCCTGGATACCAACAGCTACCCATTAGAGCTGGCAGACTACGATCTGGCCCTGGATA	905
Db	1676	-----GCCCTGGACA	1685
QY	906	CCAACACTGCTTCAGCTCCACGAGAGAAAGTGTGCGTGGCGAGCTTCATATTGACT	965
Db	1686	CCAACATATTGCTTCAGCTCCACGAGAGAAAGTGTGCTGCGGCGAGCTTCATATTGACT	1745
QY	966	TCCGGAAGGACCTGGGCTGGAATGATTTATGAAACCCAGAGGGCTACCAATTTCT	1025
Db	1746	TTCCGGAAGGACCTGGGCTGGAATGATTCACAGAGGCCCAAGGGCTACCAATTTCT	1805
QY	1026	GCGTGGGGGCTTCCTCCCTACATCTGAGGCTTAGACATCACTGATCAGCAAGGCTCTGCTC	1085
Db	1806	GCGTGGGGGCTTCCTCCCTACATTTTGAAGCCTGGACAGCAGTACAGCAAGGCTCTGCGCC	1865
QY	1086	TGTACAAACGACCAACCCGGGGCGTGGCGGGCGCGTGTGCTGTGCTCGCAGGCGCTGG	1145
Db	1866	TGTACAAACGACATTAACCCGGGGCGCTTGGCGGGCGCGTGTGCTGTGCTCGCAGGCGCTGG	1205
QY	1146	AGGCACGTGCCATGTGTACTACGTGGGCGCGCAAGCCCAAGTGTGAGCAGCTGTGCACA	1205
Db	1926	AGGCAGCTGCCATGTGTACTACGTGGGCGCGCAAGCCCAAGTGTGAGCAGCTGTGCACA	1985

QY	1206	TGATCTGGCTTCTCTGTAATGGAGCGTAGAGCCCGGCGCCGCCACAGACCCCGCCACCC	1265
Db	1986	TGATCTGGCTCTCTGTAATGGAGCTGAGAGTCCCGCCCGCCCGCCCGCCCGAG	2045
QY	1266	GGGAGGCGCGGCGCCCAACCCCGCGCGCT-----CACCGGGGCGTATTTAAGGACA	1317
Db	2046	GCGCGGCGCCACCCCGCGCGCGCGCGCTCCCTTGGCCCATAGGGGGCGTATTTAAGGACA	2105
QY	1318	TCGTGCCCCAAGGCCCACTTGGATTCGATTTAAA	1349
Db	2106	CCGTGCCCCAAGGCCCACTTGGGGGCCCATTTAA	2137

ID	Accession	Description
XX	AA015720	standard; cDNA; 2537 BP.
AC	AA015720;	
XX	U015720	(revised)
DT	25-JAN-1980	(first entry)
XX		
DE		Pre-transforming growth factor beta 1 cDNA.
XX		
KW		transforming growth factor beta 1; wound healing; recombinant production; ss.
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	5'UTR	1..841
FT		/tag= a
FT	misc_feature	37..113
FT		/tag= b
FT		/note= "GC-rich region forms stable hairpin loops; similar to structural organisation of C-myc RN could play role in mRNA stability or in regulation of transcription"
FT	CDS	842..2014
FT		/tag= c
FT		/product= pre-TGF_beta_1
FT	mat_peptide	1676..2011
FT		/tag= d
FT		/product= mature_TGF_beta_1
FT		2015..2100
FT		/tag= e
FT	repeat_region	/note= "GC-rich region; possibly responsible for the fact 3'UTR of mRNA could not be cloned as cDNA may be important for transcribtion efficiency"
FT		2019..2023
FT	repeat_unit	/tag= f
FT	TATA_signal	2094..2100
FT		/tag= g
FT		/note= "TATA-like sequence; no evidence that this functions a promoter"
FT	polyA_signal	2514..2520
FT		/tag= h
FT	misc_signal	2529..2536
FT		/tag= i
FT		/note= "consensus sequence immediately precedes polyA-tail (Benowitz et al)"
XX		
PN	U05482851-A.	
XX		
PD	09-JAN-1996.	
XX		
PF	22-MAR-1985;	85US-0715142.
XX		
PR	13-MAR-1987;	87US-0025423.
PR	22-MAR-1985;	85US-0715142.
PR	04-AUG-1989;	89US-0389929.
PR	04-MAR-1992;	92US-0848993.
PR	05-NOV-1993;	93US-0147364.

[illegible]

QY	546	GGGGTAAACCTGACAAACCGGCTGTGGGCCCCCAATGAACTACACGGAGTGGCTGTCTTTG	603
Db	1377	GGCGATACTCAGCAACCGGCTGTGGACCCCAACGCACTGCCAGAGTGGTTACTTTCTTTG	1438
QY	606	ATGTACACGGAGTTGTGGCGAGTGGCTGTGACCCGCAAGAGAGGCTATAGAGGTTTGGCC	665
Db	1437	ATGTACACGGAGTTGTGGCGAGTGGTTGAAGCGTTGAGGGGAATTGAGGGCTTTGGCC	1498
QY	666	TGAGTGGCCCACTTTCTCTGTGACAGCAAAATTAACACTTCACGTGGAAATTAACGGGT	725
Db	1497	TTAGCGCCCACTCTCTCTGTGACAGCAGGGAATTAACACTGTCAAGTGGACATCAACGGGT	1556
QY	726	TCAATTCTGGCCCGGGGGTGGACCTGGCCACCAATTCACGGATGAACCGGCTTCTCGC	785
Db	1557	TCACATACGGCCCGCGAGTGGACCTGGCCACCAATTCATGGCATGAACCGGCTTCTCTCGC	1616
QY	786	TCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACTGACACAGCTCCCGGACCCGGAG	845
Db	1617	TTCTCATGGCCACCCCGCTGGAGAGGGCCAGCATGCTCAAAAGCTCCCGGACCCGGCA -	1675
QY	846	CCCTGGATACAAACAGCTAACCCATTAGAGCTGGCAGACTACGATCTGTGGCCCTGGATA	905
Db	1676	-----GCCCTGGACA	1685
QY	906	CCAACCTACTGCTTACAGCTCCACGGAGAAAGAACTGCTGCTGGCGACCTTACATTGACT	965
Db	1686	CCAACCTATTGCTTACAGCTCCACGGAGAAAGAACTGCTGCTGGCGACCTTACATTGACT	1745
QY	966	TCCGGAGAGACCTGGGGCTGGAGTGAATTCATGAACCCCAAGGCTTACATGCCAATTTCT	1025
Db	1746	TTCCGAGAGACCTGGGGCTGGAGTGAATTCACAGAGCCCAAGGCTTACATGCCAATTTCT	1805
QY	1026	GCCCTGGGGCTTGTCCCTACATCTGAGGCTTACACTGATACAGCAAGGCTTGTGGCTC	1085
Db	1806	GGCTGGGGCTTGTCCCTACATTTTGAAGCTTGAACACGCAATGCAAGAAAGGCTTGTGGCC	1865
QY	1086	TGTACAAACGACAAACCCGGGCGCTGCGGGGCGCTGCTGCTGCTGCGCCAGAGCGCTGG	1145
Db	1866	TGTACAAACGACATTAACCCGGGCGCTGCGGGGCGCTGCTGCTGCTGCGCCAGCGCTGG	1925
QY	1146	AGCCACTGCGCCATCTGTGTACTACATGAGGGCGCGCAAGCCCAAGGTGAAGCACTGTCCACA	1205
Db	1926	AGCCGCTGCCCATCTGTGTACTACATGAGGGCGCGCAAGCCCAAGGTGAAGCACTGTCCACA	1985
QY	1206	TGATGTGCTGTCTCTGTGCAAGTCAAGTGAAGGCGCGCCCGCCACAGCGCCGCGCCACCC	1265
Db	1986	TGATGTGCTGCTCTGTGCAAGTCAAGTGAAGTTCGCGCCCGCGCCCGCCCGCGCGAG	2045
QY	1266	GGCAGGCGCGCGCCACCCCGCGCGCT-----CACGGGGCTGTATTTAAGGACA	1317
Db	2046	GCCCGGCGCCACCCCGCGCGCGCGCGCTGTGGCCATGGGGGCTGTATTTAAGGACA	2105
QY	1318	TGCTGCCCCCAAGCCACTTGGGATGGATTAATAA	1349
Db	2106	CGTGTCCCCCAAGCCACTTGGGGGCCCCCATTA	2137

FT	CDS	842...2014
FT		/*tag= a
FT	mat_peptide	1676...2011
FT		/*tag= b
FT	stem_loop	37...113
FT		/*tag= b
FT		/*note= "putative stable hairpin loop"
FT	misc_feature	2015...2100
FT		/*tag= c
FT		/*note= "GC-rich sequence"
FT	polyA_signal	2514...2520
FT		/*tag= d

Example 3; Fig 1B 1-3; 26pp; English.

CC This nucleotide sequence codes for the human transforming growth
CC factor-beta 1 precursor (preTGF-beta 1, see AAW78785). It is a
CC composite of overlapping cDNA clones isolated from different cDNA
CC libraries (placenta, A172 glioblastoma, HT1080 fibroblastoma) using
CC TGF-beta exon (see AAW52936) restriction fragments as probes.
CC The 3' region of the sequence was determined using cloned genomic
CC DNA. The invention relates to the recombinant production of
CC TGF-beta. Biologically active TGF-beta is defined as being capable
CC of inducing EGF-potentiated anchorage independent growth of target
CC cell lines and/or growth inhibition of neoplastic cell lines.
CC Nucleic acids encoding TGF-beta have been isolated and cloned into
CC vectors which are replicated in bacteria and expressed in
CC eukaryotic cells. TGF-beta recovered from transformed cells is
CC used in known therapeutic applications. TGF-beta nucleic acids are
CC also useful in diagnosis and identification of TGF-beta clones.
XX
XX Sequence 2537 BP; 475 A; 895 C; 736 G; 431 T; 0 other;

Query Match	71.6%	Score 974;	DB 19;	Length 2537;
Best local Similarity	84.5%	Pred. No. 4.6e-187;		
Matches 1143; Conservative	0;	Mismatches 150;	Indels 59;	Gaps 2

QY b CCGAGATGGACGCTTTCGGGGCTCGGGCTCTTCCGCGTGTGCGCGCGCTGGTGGTGC 65
 Db 837 CCCCCAGCCGCGCTCCGGGCTGCGGCTGCTCCGCTGTCTACCGCGCTGCTGTGGCTAC 896
 QY 66 TAGTGTGACGCGCTGGCGCGCGCGCGCGCGAGCTGCCACCTGGCAAGACCATCGACATGG 125
 Db 897 TGGTGTGACGCGCTGGCGCGCGCGCGCGCGAGCTATCCACCTGCAAGACTATCGACATGG 956
 QY 126 ACCTGGTGAAGCGGAAGCGCATATCGAAGCGCATTTTCGGCGCCAGATTGTTCACAGCTTGGGC 185
 Db 957 ACGAGTGAAGCGGAAGCGCATATCGAAGCGCATTCGGCGCGCGAGTATCTGTTCACAGCTTGGCGC 1016

QY	186	TTGCAACCCCCCGAGCGAGGGGAGCTGCGCGCCCGCGCTGCTGTCAGGACGATCTGG	245
Db	1017	TCGCGACACCCCCCGAGCGAGGGGAGGTGGCCCGCGCGCTGCTGCGAGCGCTGCTCG	1076
QY	246	CTCTTTTCAACAGATGATCCCGGACCGGGGTAGCGCGGGGAAAGTGTGCAGCCGAGCCGAGC	305
Db	1077	CCCTGTACAAAGAGCAACCCCGGACCGGGGTGGCCCGGGGAGAGTGCAGAACCCGGAGCCCGAGC	1136
QY	306	CAGAGCGGGACTACTACGCCAAGAGGTACCCCGCTGCTTAATGGTGGAAAGCGGCAAC	365
Db	1137	CTGAGGCGGCACTACTACGCCAAGAGGTACCCCGCTGCTTAATGGTGGAAAGCGGCAAC	1196
QY	366	AAATCTATGATTAATTTAAAGGGGACCCCCCAGCTTATATGCTGTGTCAACACGCTGG	425
Db	1197	AAATCTATGACAACTTTCACGACGAGATACACAGCATATATATGTTCTTCAACACATCAG	1256
QY	426	AGCTCGGGGAGCGGTGCGGGAACCTGTATTGCTCTCTCGGGCAGAGCTGGCGCTGCTGA	485
Db	1257	AGCTCCGAGAGCGGTACTACACCCCGTGTCTCTCCCGGGCAGAGCGCTGTGCTGA	1316
QY	486	GGCTCAAGTTTAAAGTGGAGGACGCGTGAGGCTATTACAGAAATACAGCATGATTCCT	545
Db	1317	GGCTCAAGTTTAAAGTGGAGGACGCGTGAGGCTATTACAGAAATACAGCATGATTCCT	1376
QY	546	GGCGCTACTCTAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGCTTTG	605
Db	1377	GGCGATTACTCAGCAACCGGCTGCTGGCACCCAGAGCTCGCAGAGTGGTATTCTTTTG	1436
QY	606	ATGTACCGGAGTGTGGGGCAGTGGCTGAACCCGAGAGGCTATTAGGGGTTTTGCGC	665
Db	1437	ATGTACCGGAGTGTGGGGCAGTGGCTGAACCCGAGAGGCTATTAGGGGTTTTGCGC	1496
QY	666	TCAGTGCCCACTCTTCTCTGTGACAGCAAAAGATTAACACACTCCACGTGAATTAACGGGT	725
Db	1497	TTAGGGCCACAGTCTCTGTGTGACACAGGAGTAAACACTGCAAGTGGACATCAAGGGGT	1556
QY	726	TCAAATTCGGCGCGCGGGGGTGACTGGGCAACCATTCAGCGCATGAACCGCGCTTCTCG	785
Db	1557	TCACATCCGGCGCGCGAGGTGTGACTGGCCACCATTCTATGSCATGAACCGGCTTCTCTCG	1616
QY	786	TCCTCATATGGCCACCCCGCTGGAGAGGGCCACACCTGCAGAGCTCCGGCACCGCGCAG	845
Db	1617	TTCTCATATGGCCACCCCGCTGGAGAGGGCCACACATCTGCAAAAGCTCCCGCACCGCGCA	1675
QY	846	CCCTGTGATACCAACAGCTACCATACAGCTGCACAGTACTGCTGGCCCTGGATA	905
Db	1676	-----GCCCCGGACA	1685
QY	906	CCAATCTAGCTTCAAGTCCACAGAGAAACATGCTGCTGCGGACGCTTACATTTGACT	965
Db	1686	CCAATCTATTTGCTTCAAGTCCACAGAGAAACATGCTGCTGCGGACGCTTACATTTGACT	1745
QY	966	TCGCGAAGGACCTGGGCTGGAAAGTGAATTCATGTAACCCAAAGGCTTACATGCCAATTTCT	1025
Db	1746	TCGCGAAGGACCTGGGCTGGAAAGTGAATTCATGTAACCCAAAGGCTTACATGCCAATTTCT	1805
QY	1026	GGCTGGGGGCGCTGCCCTCACTCTGAGGCTTAACACTGATCAGAGAAAGTCTTGCTC	1085
Db	1806	GGCTGGGGGCGCTGCCCTCACTCTGAGGCTTGACACAGCATGATGACGAAGGCTTGCTC	1885
QY	1086	TGTACAAACAGCAACAACCCGGGCGCTGGCGGGCGCTGCTGCTGCGCAGGCGCTGG	1145
Db	1866	TGTACAAACAGCAATACCCGGGCGCTGGCGGGCGCTGCTGCTGCTGCGCAGGCGCTGG	1925
QY	1146	AGGCAATGGCCATCGTGTACTACTGGGGCGCAAGCCAAAGGTGAGACAGCTGTCCACA	1205
Db	1926	AGGCGTGGCCATCGTGTACTACTGGGGCGCAAGCCAAAGGTGAGACAGCTGTCCACA	1985
QY	1206	TGATTCGTGGCTTCTCTCAAGTGTGAGGAGGAGCCCGCCGACACAGACCCCGCCACCC	1265
Db	1986	TGATTCGTGGCTTCTCTCAAGTGTGAGGAGTCCCGCCCGCCGCGCCCGCCGAG	2045
QY	1266	GGCAGGCGCGGCCCCACACCCCGCGCT-----CACCGGGGCTGTATTTAAGGACA	1317

Db	2046	GCCTGGGCCCCCAGCCCGGCCCCCGCCCGCTGCTGGCCATGAGGGGGCTGTATTAAAGACA	2105
QY	1318	TGCTGCCCCAAGCCCACTTGGGATCGATTTAAA	1349
Db	2106	CCGTGCCCCAAGCCCACTTGGGATCGATTTAAA	2137
RESULT 8			
AAQ03268			
ID	AAQ03268	standard; DNA; 1561 BP.	
XX	AC	AAQ03268;	
XX	AAQ03268;		
XX	12-AUG-1990	(first entry)	
XX	Simian transforming growth factor-beta cDNA.		
DE	Transforming growth factor-beta; psoriasis; TGF-beta; ss.		
KW	Monkey.		
XX	Key	Location/Qualifiers	
XX	sig_peptide	283..324	
FT	mat_peptide	/*tag= a	
FT		1096..1431	
FT		/*tag= b	
FT		/product=human transforming growth factor-beta	
XX	EP353772-A.		
XX	07-FEB-1990.		
XX	04-AUG-1989;	89EP-0114458.	
XX	05-AUG-1988;	88US-0229133.	
XX	(ONCO-) ONCOGEN LTD PARTNER.		
XX	Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;		
XX	WPI; 1990-038499/06.		
DR	P-PSDB; AAR03743.		
XX	Inhibition of proliferation of epidermal cells -		
PT	used to treat psoriasis by contacting cells with compositions		
PT	containing transforming growth factor-beta.		
XX	Disclosure; fig 1; 20pp; English.		
XX	TGF-beta may be used in the treatment of hyperplasia		
CC	associated with acanthosis-categorised skin diseases, and		
CC	in alleviating psoriatic symptoms associated with cytokine-		
CC	induced phenomena. See also AA003269 and AAR03750.		
XX	Sequence 1561 BP; 301 A; 547 C; 446 G; 267 T; 0 other;		
QY	Query Match	71.3%; Score 971; DB 11; Length 1561;	
Db	Best Local Similarity	84.8%; Pred. No. 1.7e-186;	
	Matches 1148; Conservative	0; Mismatches 145; Indels 60; Gaps	
QY	6	CCGAGATGGGCGCTTGGGGGCTGGGCTCTTGGCGTGTGCTGCCGCTGCTGC	65
Db	257	CCGCCATGGCGCCCTCCCGGCGCTGCTGCTGCCGCTGCTGCCTGCTGCTAC	316
QY	66	TAGTGTGACGCTTGGCGCGCGCGCGCGCGAGTGTGCACCTGCAGACATGACATG	125
Db	317	TGTGTGTGAGCGCTTACCGCGCGCGCGCGAGACTTATCCATGACATGACATG	376
QY	126	AGCTGTGAGCGGAGAGCGCATGAGGCGCATTTGCGCGCCAGATTCTGTCCAACTTGGC	185
Db	377	AGCTGTGAGCGGAGAGCGCATGAGGCGCATTTGCGCGCCAGATTCTGTCCAACTTGGC	436

QY	186	TTMCCAGCCCCCGAGCCAGGGGGACGTGCCGCCGCCCTGCTGAGGCATGCTGG	245
Db	437	TCGCACAGCCCCCGAGCCAGGGGGAGGTGCCGCCGCCCTGCTGCCAGGCCGTCTCG	496
QY	246	CTCTTTACACAGTACCCGGACCGGGGTAGCCGGGGAAAGTGCACCCGGAGCCCGAGC	305
Db	497	CCCTGTACACAGCACCCCGGACCCGGGTGGCCGGGGAGATGTCGAGCCGGAGCCGAAC	556
QY	306	CAGAGCGGACCTACCTACGCCAAGGAGTCAACCGCGTCTAATGGTTGAAAAAGCGCAAC	365
Db	557	CGAGAGCCGCACTACAGCCAGAGAGGTCAACCCCGCTGCTAATGGTGAACCAACG	616
QY	366	AAATCTATGATTAATTAATCAAGGGCAACCCCAACCTTATATATGGTGTCAACAGCTGG	425
Db	617	AAATCTATGCAAGTTAAAGACAGAGCAACACACATATATATGTCTTCAACACATATAG	676
QY	426	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGAGAGCTGGCCCTGTGA	485
Db	677	AGCTCCGGAAGACAGTACCTGAACCTGTATTGCTCTCCCGGGCAGAGCTGGCTGTGTA	736
QY	486	GGCTCAAGTTAAAGTGGACAGACGACGTGGAGCTATACAGAAATACAGCAATATCTCT	545
Db	737	GGCTCAAGTTAAAGTGGACAGACGATGTGAGCTGTACCAAAATACAGCAAACTTCTCT	796
QY	546	GGCGCTACCTCAGCAACCCGCGTCTGTGGCCCACTGATCAACCGAGAGCGCTGTCCTTG	605
Db	797	GGGATACCTCAGCAACCCGCGTCTGTGGCCCACTGATCAACCGAGAGCGTGTCTTTTG	856
QY	606	ATGTACCCGGAGTGTGTGCGGCACTGGCTGTACCCGAGAGAGGCTATAGAGGTTTGGCC	665
Db	857	ATGTACCCGGAGTGTGTGCGGCACTGGTGTGAGCGCGGAGGGGAAATTGAGGCTTTCGCC	916
QY	666	TCAGTCCCACTTCTCTCTGACAGCAAAATATACACACTCCAGCTGGAAATTAAACGGGT	725
Db	917	TTAGGCGCCACTCTCTCTGTGACAGCAAAATATACACTGCAAGTGGACATCAACGGGT	976
QY	726	TCATTTCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAAACCGGCCCTTCGCG	785
Db	977	TCACTACCGCGCGCCAGAGTGACCTGGCCCAATTCATGGCATGAACCGGCTTTCCTGCG	1036
QY	786	TCCCTATGGGCAACCCGCGTGGAGAGGGCCAGACACGACAGTCCCGGACCGCGGAG	845
Db	1037	TTCTCTATGGGCCAACCCGCTGAGAGGGCCCAACATCTGCAAAAGTCCCGGACCGCGCA	1095
QY	846	CCCTGGATTCCAAACAGCTAACCCATACGACGTGCTAGACTCTGTGGCCCTGTGATA	905
Db	1096	-----GCCCTGGACA	1105
QY	906	CCACGACTGCTTACGCTCACGCGAGAAAGACGTGCGCGGCACTCTACATTTGACT	965
Db	1106	CCACTACTGCTTACGCTCACGCGAAGAAAGACGTGCGCGGCACTGTATATTGACT	1165
QY	966	TCCGGAAGGACCTGGGCTGGAGTGGATTCTATGAAACCAAGGGGTATACATGCCAAATTC	1025
Db	1166	TCCGGAAGGACCTGGGCTGGAGTGGATTCTATGATCCAGAGCCCAAGGGGTATACATTTCT	1225
QY	1026	GGCTGGGGGCGTGCCTTCATCTGAGAGCTTAGACACTAGTACAGTAAGTCTTGCTC	1085
Db	1226	GGCTGGGGGCGTGCCTTCATCTGAGAGCTTGAGAGCTTGACAGCAAGTGTCTTGCC	1285
QY	1086	TGTACAAACGACACAACCCGGGCGCTCGCGGGCGCGCTGCTGCTGCGCCAGCGCTGG	1145
Db	1286	TGTACAAACGACATAAACCCGGGCGCTCGGGCGCGCGTCTGCTGCTGCGCAGGCGCTGG	1345
QY	1146	AGCCACTGGCCATCTGTGTACTATAGTGGCCCGCAAGCCCAAGGTGAGACAGCTGTCCAA	1205
Db	1346	AGCCACTGGCCATCTGTGTACTATAGTGGCCCGCAAGCCCAAGGTGAGACAGCTGTCCAA	1405
QY	1206	TGATGCTGCTTCTGCAAGTGAAGTGAAGCCCGCGCCCGCCACAGCCCGCCGCCACCC	1265
Db	1406	TGATGCTGCTGCTTCTGCAAAATGCAAGTGAAGCCCGCGCCCGCCACCCCGCCGAC	1465
QY	1266	GGCAGGCGGCGCCGCCGCCCGCGCT-----CACCGGGGCTGTATTTAAGGACA	1317

[illegible]

Prod. of simian transforming growth factor beta-1 - by culturing
transfected eucaryotic cells, and new precursor proteins, useful for
treating tumours.
XX
PS Disclosure: ; pp: English.
CC The cdna is prep'd. from African green monkey cell line BSC-40 and is
expressed in eukaryotic cells in plasmid pSV2. There is 100% homology
between mature simian and human TGF-beta 1. The plasmid also contains
the SV40 promoter and a selection marker, esp. DHFR.
CC
XX

Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;

Query Match 71.1%; Score 967.6; DB 9; Length 1560;
Best Local Similarity 84.9%; Pred. No. 8.5e-186;
Matches 1144; Conservative 0; Mismatches 144; Indels 60; Gaps 3;

11 ATGGCCCTTCGGGGCTGGCGCTCTTGGCGCTGCTGCTGCGGCTGCTGCTGCTAGTG 70
11 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
261 ATGCCCCCTCCGGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 320
71 CTGAGCGCTGGCGGGCGGGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 130
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
321 CTGAGCGCTGAGCGGGCGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 380
131 GTGAACCGGAAGCGCATCGAGGCGGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 190
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 GTGAACCGGAAGCGCATCGAGGCGGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 440
191 AGCCCCCGGAGCGAGGGGGAGCTGCGCGCGCGCGCGCGCGCGCTGCTGAGAGGCTGCT 250
441 AGCCCCCGGAGCGAGGGGGAGCTGCGCGCGCGCGCGCGCGCGCTGCTGAGAGGCTG 500
251 TACAACAGTACCCGCGAGCGAGGCTGCGCGCGCGCGCGCGCGCGCTGCTGAGAGGCTG 310
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
501 TACAACAGGACCGCGCGAGCGAGGCTGCGCGCGCGCGCGCGCGCGCTGCTGAGAGGCTG 560
311 GCGGACTACTACCGCAAGAGGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 370
561 GCGGACTACTACCGCAAGAGGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 620
371 TATGATTAATTCAGAGGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 430
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
621 TATGATTAATTCAGAGGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 680
431 CGGGAAGCGGCTGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 490
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
681 CGGGAAGCGGCTGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 740
491 AAGTTAAATGAGAGCGAGCGAGCTGATACCAAGAAATACAGAAATGATTCCTGGCGG 550
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
741 AAGTTAAATGAGAGCGAGCGAGCTGATACCAAGAAATACAGAAATGATTCCTGGCGG 800
551 TACCTGAGCAACCGGCTGCTGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 610
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
801 TACCTGAGCAACCGGCTGCTGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 860
611 ACCGAGTGTGCGCGAGTGCTGACCGCGAGAGAGGCTATAGAGGCTTTCGCTCACT 670
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
861 ACCGAGTGTGCGCGAGTGCTGACCGCGAGAGAGGCTATAGAGGCTTTCGCTCACT 920
671 GCCGACTCTTCTGACAGAAAGATTAACACCTCCACAGTGGAAATTAACGGCTTCAT 730
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
921 GCCGACTCTTCTGACAGAAAGATTAACACCTCCACAGTGGAAATTAACGGCTTCAT 980
731 TCTGCGCGCGGCTGAGCTGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 790
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
981 ACCGCGCGCGGAGTGACCTGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 1040
791 ATGGCCACCGCGCTGAGAGGGCGCGAGCACTGCAAGCTCCCGGCGAGCGCGGCGCTG 850
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1041 ATGGCCACCGCGCTGAGAGGGCGCGAGCACTGCAAGCTCCCGGCGAGCGCGGAG----- 1095

QY 851 GATACCAACAGCTACCATACGAGCTGCCAGACTACGACTCTCTGCGCTGATACCAAC 910
DB 1096 ----- CCTGGACACCAAC 1109
QY 911 TACTGCTTACCTCCAGGAGAGACTGCTGCTGCGGAGCTGCTACATGACTCCGG 970
DB 1110 TATGCTTACCTCCAGGAGAGACTGCTGCTGCGGAGCTGCTACATGACTCCGG 1169
QY 971 AAGGAGCTGAGCTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1030
DB 1170 AAGGAGCTGAGCTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1229
QY 1031 GGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1090
DB 1230 GGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1289
QY 1091 AAGGAGCTGAGCTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1150
DB 1290 AAGGAGCTGAGCTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1349
QY 1151 CTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1210
DB 1350 CTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1409
QY 1211 GTGCGCTTCTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1270
DB 1410 GTGCGCTTCTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1469
QY 1271 GCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1321
DB 1470 GCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1529
QY 1322 GCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1349
DB 1530 GCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1579
RESULT 13
AA003508
ID AA003508 standard; DNA: 1560 BP.
XX
AC AA003508;
XX
AC
XX
DT 14-AUG-1990 (first entry)
XX
DE Simian Transforming growth factor - Beta1.
XX
KW HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
XX
KW factors; ds.
XX
FH Key
XX
FT CDS
XX
FT mat_peptide
XX
PN EP356935-A.
XX
PD 07-MAR-1990.
XX
PF 25-AUG-1989; 89EP-0115719.
XX
PR 25-AUG-1988; 88US-0236698.
XX
PA (ONCO-) ONCOGEN LTD PARTNER.
XX
PI Brankovan V, Llobulin M, Purchio A;
XX
DR WPI: 1990-068723/10.
XX
DR P-PSDB: AAR05663.
XX
PT Comps. contg. transforming growth factor beta -
used for inhibitions of HIV infection and replication in vivo.

XX (Pfizer) Pfizer Ltd.
 PA (Pfizer) Pfizer Inc.
 XX
 PI Davies MJ, Huggins JP, McIntosh FS, Occleston NL;
 XX
 DR WPI: 2001-418351/44.
 P-PSDB: AAB84601.
 XX
 PT Composition for the treatment of damaged tissue i.e. chronic wounds and
 PT dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
 factor -
 XX
 PS Disclosure: Page 547; 572pp; English.
 XX
 CC The specification describes a pharmaceutical composition, comprising
 CC a growth factor, an inhibitor agent, i.e. a protease. The inhibitor
 CC agent inhibits the action of at least one specific adverse protein,
 CC i.e. a protease, that is upregulated in a damaged tissue such as a
 CC wound environment. Growth factors which are included in the composition
 CC of the invention are platelet-derived growth factor (PDGF), fibroblast
 CC growth factor (FGF), connective tissue derived growth factor (CTGF),
 CC keratinocyte-derived growth factor (KGF), transforming growth
 CC factor-beta (TGF-beta), granulocyte macrophage colony stimulating factor
 CC (GM-CSF), epidermal growth factor (EGF), vascular endothelial growth
 CC factor (VEGF), and chrysalin. Inhibitors which are included in the
 CC composition of the invention include inhibitors of urokinase-type
 CC plasminogen activator (uPA) and matrix metalloproteinase (MMP). The
 CC composition is useful for the treatment of chronic damaged tissue, i.e.
 CC wounds and dermal ulcers. The present sequence encodes a human TGF-beta,
 CC and is used to produce the composition of the invention.
 XX
 XX Sequence 2745 BP; 527 A; 938 C; 801 G; 479 T; 0 other;
 Query Match 71.0%; Score 965.8; DB 22; Length 2745;
 Best Local Similarity 84.6%; Pred. No. 2,1e-185;
 Matches 1146; Conservative 0; Mismatches 147; Indels 62; Gaps 3;

QY 543 CCTGGCGTACTCTACAGCAACCGGCTGCTGCCCCCAGTACTACCGGAGTGGCTGTCT 602
 Db 1377 CCTGGGAGTACTCTACAGCAACCGGCTGCTGCCCCCAGTACTACCGGAGTGGCTGTCT 1436
 QY 603 TTGATGTACCGGAGTTTGGCGAGTGGTGGTGGCGGAGGAGGCTATAGAGGTTTC 662
 Db 1437 TTGATGTACCGGAGTTTGGCGAGTGGTGGTGGCGGAGGAGGCTATAGAGGTTTC 1496
 QY 663 GCTTCACTGCGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 722
 Db 1497 GCTTCACTGCGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1556
 QY 723 GGTTCATTTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 782
 Db 1557 GGTTCATTTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1616
 QY 783 TGTCTCTATGGCCACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 842
 Db 1617 TGTCTCTATGGCCACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1676
 QY 843 GAGCCCTGGATTCACAGAGTACCCATACGAGCTGCGGAGACTACGCTCTGGCCCTGG 902
 Db 1677 GA-----GCGCTGG 1685
 QY 903 ATACCACTACTGTTCAAGCTCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 962
 Db 1686 ACACCACTATTGTTCAAGCTCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1745
 QY 963 ACTTCGGAAG 1022
 Db 1746 ACTTCGGAAG 1805
 QY 1023 TCTGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1082
 Db 1806 TCTGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1865
 QY 1083 CTCTGTACACAGCAGCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1142
 Db 1866 CCTGTACACAGCAGCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1925
 QY 1143 TGAAGCAGTCCCATCTGTACTAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1202
 Db 1926 TGAAGCAGTCCCATCTGTACTAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1985
 QY 1203 ACATGATGCTGCTCTCTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1262
 Db 1986 ACATGATGCTGCTCTCTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2045
 QY 1263 CCCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1314
 Db 2046 CAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2105
 QY 1315 ACATGCTGCCCAAGCCACTTTGGAGTGAATTA 1349
 Db 2106 ACACGCTGCCCAAGCCACTTTGGAGTGAATTA 2140

Search completed: April 15, 2003, 10:07:59
 Job time : 420 secs

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(c) 1993 - 2003 CompuGen Ltd.

alc search, using sw model

April 15, 2003, 10:33:16 ; Search time 70 seconds (without alignments)

5962.672 Million cell updates/sec

S-10-017-372E-36

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IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

41362 seqs, 153338381 residues

its satisfying chosen parameters: 8827224

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length: 0
length: 2000000000000
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Minimum Match	0%
Maximum Match	100%

Listing first 45 summaries

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Issued_patents_NA: *
/can2 6/ntodata/1/ina/5A COMB seq.*
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	978.8	71.9	2537	6	516051.1	Patent No. 516051
2	970.8	71.3	1560	1	US-07-669-171-1	Sequence 1, Appl
3	965.8	71.0	2745	4	US-09-661-753-28	Sequence 28, Appl
4	965.8	71.0	2745	5	PCT-US94-03705-3	Sequence 3, Appl
5	922.6	67.8	1569	1	US-07-669-171-3	Sequence 3, Appl
6	847	62.8	2094	4	US-09-661-753-1	Sequence 1, Appl
7	827.4	60.8	1585	4	US-09-661-753-27	Sequence 27, Appl
8	773	56.8	2207	6	5221620-3	Patent No. 5221620
9	310.2	22.8	339	1	US-08-470-837-29	Sequence 29, Appl
10	308.6	22.7	339	1	US-08-486-0578-1	Sequence 1, Appl
11	308.6	22.7	339	2	US-08-789-588-1	Sequence 1, Appl
12	308.6	22.7	339	3	US-09-123-233-1	Sequence 1, Appl
13	308.2	22.6	337	4	US-08-868-452-29	Sequence 29, Appl
14	248	18.2	2671	6	5168051-9	Patent No. 5168051
15	245.8	18.1	2529	5	PCT-US91-04541-1	Sequence 1, Appl
16	245.8	18.1	2529	6	5262319-1	Patent No. 5262319
17	245.8	18.1	2574	4	US-09-380-662-20	Sequence 20, Appl
18	229.4	16.7	336	3	US-09-123-233-7	Sequence 7, Appl
19	229.4	15.4	339	1	US-08-486-0578-3	Sequence 3, Appl
20	209.4	15.4	339	1	US-08-470-837-33	Sequence 33, Appl
21	209.4	15.4	338	2	US-08-789-588-3	Sequence 3, Appl
22	209.4	15.4	339	3	US-09-123-233-5	Sequence 5, Appl
23	209.4	15.4	339	4	US-09-000-0694-1	Sequence 1, Appl
24	209.4	15.4	339	4	US-08-868-452-33	Sequence 33, Appl
25	202	14.8	2173	6	5168051-10	Patent No. 5168051
26	182.4	13.4	336	3	US-09-123-233-11	Sequence 11, Appl
27	160.8	13.3	336	3	US-09-123-233-9	Sequence 9, Appl

45	50.4	3.7	894	6	5167076-3	Patent No. 5167076
44	50.4	3.7	894	1	US-07-764-731B-3	Sequence 3, Appl.
43	50.4	3.7	894	1	US-07-764-731B-3	Sequence 254, Appl.
42	50.4	3.7	658	2	US-08-621-803-254	Sequence 254, Appl.
41	62.6	4.6	5578	1	US-08-081-610-2	Sequence 2, Appl.
40	68.8	5.1	110	5	PCr-US81-02331-11	Sequence 11, Appl.
39	68.8	5.1	110	2	US-08-431-333-11	Sequence 11, Appl.
38	68.8	5.1	110	2	US-07-668-648-11	Sequence 11, Appl.
37	68.8	5.1	110	1	US-07-668-648-11	Sequence 11, Appl.
36	130.4	9.6	339	6	US-08-668-452-31	Sequence 51, Appl.
35	140	10.3	975	6	5168051-3	Patent No. 5168051
34	155	11.4	2569	6	5221620-1	Patent No. 5221620
33	158.2	11.6	1695	3	PCr-US64-03705-4	Sequence 4, Appl.
32	158.2	11.6	339	3	US-09-123-233-3	Sequence 3, Appl.
31	158.2	11.6	339	2	US-08-789-588-2	Sequence 2, Appl.
30	158.2	11.6	339	1	US-08-470-837-31	Sequence 31, Appl.
29	158.2	11.6	339	1	US-08-466-057B-2	Sequence 2, Appl.
28	179.8	13.2	4267	4	US-09-661-753-47	Sequence 47, Appl.

ALIGNMENTS

```

RESULT 1
5168051-1
: Patent No. 5168051
: APPLICANT: DERYNCK, RIK M. A.; GOEDEL, DAVID V.
: TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF- $\beta$  ITS USES
: NUMBER OF SEQUENCES: 21
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/389,929
: FILING DATE: 04-AUG-1989
: SEQ. ID NO.: 1
: LENGTH: 2537
5168051-1

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Query Match	71.9%;	Score 978.8;	DB 6;	Length 2537;
Best Local Similarity	84.8%;	Pred. No. 1.7e-198;		

QY	6	CCGAGATGCGCCCTTCGCGGCGCTGCGGCTCTTCCCGCTGCTGCTGCGGCTCTGCTGCGCTG	65
Dp	837	CCCCCATCCGCCCTTCGCGGCTGCGGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	896
QY	66	TAGTGTGACGCGCTGCG	1255
Dp	897	TGTGTGTGACGCCCTGCG	956
QY	126	AGCTGTGTGAAGCGGAAGCGCATTCGAGGCGCATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	185
Dp	957	AGCTGTGTGAAGCGGAAGCGCATTCGAGGCGCGCATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	101
QY	186	TTGCGAGCG	245
Dp	1017	TGCGAGCG	107
QY	246	CTCTTTACACAGTACCCG	305
Dp	1077	CCCTGTACACAGTACCCG	113
QY	306	CAGAGGCGGACTTACTACGCGCAAGGAGTCAACCGCGTAAATGTTGGTGAAGGCGGCAAC	365
Dp	1137	CTGAGGCGGACTTACTACGCGCAAGGAGTCAACCGCGCGTAAATGTTGGTGAAGGCGGCAACG	119
QY	366	AAATCTATGATAAATTCAAGGGGCAACCCCGACAGCTTATATGCTGTTCAACACGTGCG	425
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QY	426	AGCTCGGGGAGCGGTGGCGGGAACCTGTATGTGCTTCGCGGCGAGAGCTCGGCTGCTGA	485
Dp	1257	AGCTCGGGGAGCGGTGTGCTGAACCGCGTGTGCTTCGCGGCGAGAGCTCGGCTGCTGCTGA	131
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546 GGGGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTACTCACCAGAGTGGCTCTTGG 605
1377 GGGGATACCTCAGCAACCGGCTGCTGGCCCCCAGTACTCACCAGAGTGGCTCTTGG 1436
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1437 ATGTCAACGGAGTGTGTGCGGAGTGGCTGACCCCGCAGAGAGCTATAGAGGGTTTCGCC 1496
666 TCAGTGGCCACTTCTCTCTGAGACGAAAGATACACACTCCACGTGGAATTAACGGGT 725
1497 TTAGCGCCCACTGCTCTCTGAGACGAGGATTAACACACTGCAAGTGGAGATCAACGGGT 1556
726 TCATTTCTGGCCCGCGGGGTGACCTGGCCACATTCACGAGCANTGAACCGGCTTCTGTC 785
1557 TCATTTCTGGCCCGCGGGGTGACCTGGCCACATTCACGAGCANTGAACCGGCTTCTGTC 1616
786 TCCTCATGGCCACCCGCTGGAGAGGGCCACGACCTGACACACTCCCGCAGACCGCGAG 845
1617 TTCTCATGGCCACCCGCTGGAGAGGGCCACGACCTGACACACTCCCGCAGACCGCGAG 1675
846 CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTGGCCCTGGATA 905
1676 -----GCCCTGGACA 1685
906 CCAACTCTGCTTTCAGCTCCACGAGAGAACTGCTGGCGGAGCTCTACATTTAGT 965
1686 CCAACTCTGCTTTCAGCTCCACGAGAGAACTGCTGGCGGAGCTCTACATTTAGT 1745
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1746 TCCGGAAGAACCTGGCTGGAGTGGATTCATGAACCAAGGGCTACATTCCTTCT 1805
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1926 AGCCACTGCGCATGTGTACTACTGTGGGCGCGCAAGCCCAAGTGGAGAGCTTCCAACA 1985
1206 TGAATGCGCTTCTCTGCAAGTGAAGTGAAGGCGCGCGCGCGCGCGCGCGCGCG 1265
1986 TGAATGCGCTTCTCTGCAAGTGAAGTGAAGGCGCGCGCGCGCGCGCGCGCGCG 2045
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1318 TCGTGGCCCAAGCCACTTGGGATCGATTAA 1349
2106 CCGTGGCCCAAGCCACTTGGGATCGATTAA 2137

RESULT 2
US-07-669-171-1
Sequence 1, Application US/07669171
Patent No. 5304541

GENERAL INFORMATION:
APPLICANT: PURCHIO, ANTHONY F.
APPLICANT: MADISEN, LINDA
APPLICANT: MERRIN, JUNE RAE
TITLE OF INVENTION: TGF- β 1/D2: A NOVEL CHIMERIC TRANSFORMING
GROWTH FACTOR-BETA
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS

STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: N.Y.
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/669,171
FILING DATE: 19910314
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-159-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 261..1430
US-07-669-171-1
Query Match 71.3%; Score 970.8; DB 1; Length 1560;
Best Local Similarity 85.0%; Pred. No. 8e-197;
Matches 1146; Conservative 0; Mismatches 142; Indels 60; Gaps 3;
11 ATGGCGCTTGGGGGCTGGGCTCTTGGCGCTGCTGCTGCGGCTGCTGCTGCTAGTG 70
261 ATGGCGCTTGGGGGCTGGGCTCTTGGCGCTGCTGCTGCGGCTGCTGCTGCTAGTG 320
71 CTGAGGCTTGGGGGCTGGGCTCTTGGCGCTGCTGCTGCGGCTGCTGCTGCTAGTG 130
321 CTGAGGCTTGGGGGCTGGGCTCTTGGCGCTGCTGCTGCGGCTGCTGCTGCTAGTG 380
131 GTGAAGCGGAACGCAATCGAGGCTTGGCGGCTGCTGCTGCGGCTGCTGCTGCTAGTG 190
381 GTGAAGCGGAACGCAATCGAGGCTTGGCGGCTGCTGCTGCGGCTGCTGCTGCTAGTG 440
191 AGCCCCCGAGCGAGGGGAGTGGCGGCGCGCGCTGCTGCTGCGGCTGCTGCTGCTAGTG 250
441 AGCCCCCGAGCGAGGGGAGTGGCGGCGCGCGCTGCTGCTGCGGCTGCTGCTGCTAGTG 500
251 TACACAGTACCGCGGAGCGGAGTGGCGGCGCGCGCTGCTGCTGCGGCTGCTGCTGCTAGTG 310
501 TACACAGTACCGCGGAGCGGAGTGGCGGCGCGCGCTGCTGCTGCGGCTGCTGCTGCTAGTG 560
311 GCGGACTACTACGCGCAAGAGGTACCGCGGCTGCTGCTGCGGCTGCTGCTGCTAGTG 370
561 GCGGACTACTACGCGCAAGAGGTACCGCGGCTGCTGCTGCGGCTGCTGCTGCTAGTG 620
371 TATGATTAATTAAGGCGACCCCGCAGAGTGTATATGTGTTCAACAGCTGCGAGCTG 430
621 TATGATTAATTAAGGCGACCCCGCAGAGTGTATATGTGTTCAACAGCTGCGAGCTG 680
431 GCGGAGGCGGTCGCGGAGCTGCTGCTGCTGCGGCGAGAGCTGCGGCTGCTGCTGCTAGTG 490
681 GCGGAGGCGGTCGCGGAGCTGCTGCTGCTGCGGCGAGAGCTGCGGCTGCTGCTGCTAGTG 740
491 AAGTTAAAGTGGAGAGCAGCTGAGCTATACAGAAATACAGCAATTCCTGGGCGC 550
741 AAGTTAAAGTGGAGAGCAGCTGAGCTGATACAGAAATACAGCAATTCCTGGGCGA 800

551 TACCTCAGCAACCGGCTGCTGACCCCGCAGTACATCCCGAGTGGCTGCTCTTGAATGTC 610
801 TACCTCAGCAACCGGCTGCTGACCCCGCAGTACATCCCGAGTGGCTGCTCTTGAATGTC 860
611 ACCGGAATTTGGCGCAAGTGGTGAACCCCGCAGAGAGGCTATAGAGGCTTTGGCCCTCAGT 670
861 ACCGGAATTTGGCGCAAGTGGTGAACCCCGCAGAGAGGCTATAGAGGCTTTGGCCCTCAGT 920
671 GCCCACTCTCTCTGACAGCAAGATTAACACTCCACGTCCAGTAAATTAACGGGTTCAAT 730
921 GCCCACTCTCTCTGACAGCAAGATTAACACTCCACGTCCAGTAAATTAACGGGTTCAAT 980
731 TCTGGCCGCGGCGGAGTACCTGGCCACATTCACGCAATGACCGGCTTCTGCTCTCTC 790
981 ACCGGAATTTGGCGCAAGTGGTGAACCCCGCAGAGAGGCTATAGAGGCTTTGGCCCTCAGT 1040
791 ATGGCCACCCCGCTGAGAGAGGCGCCAGCACTCCAGCTCCGCGCAGCCGAGCCCTG 850
1041 ATGGCCACCCCGCTGAGAGAGGCGCCAGCACTCCAGCTCCGCGCAGCCGAGCCCTG 1095
851 GATACCAACAGCTACCATACAGAGTGCAGACTAGCATCTCTGCGCTGGATACCAAC 910
1096 -----CCCTGGACACCAAC 1109
911 TACTGCTTACGCTCCACGAGAAAGAACTGCTGGTGGGCACTCTACATTAAGCTTCGCG 970
1110 TACTGCTTACGCTCCACGAGAAAGAACTGCTGGTGGGCACTCTACATTAAGCTTCGCG 1169
971 AAGGACTGGGCTGGAAGTGGATTCATGAACCCCAAGGCTACCATGCAATTTCTGCTG 1030
1170 AAGGACTGGGCTGGAAGTGGATTCATGAACCCCAAGGCTACCATGCAATTTCTGCTG 1229
1031 GGGCCCTGCTCCATCATCTGAGCTGAGACCTAGACACTGACAGCAAGGCTCTGCTCTGAC 1090
1230 GGGCCCTGCTCCATCATCTGAGCTGAGACCTAGACACTGACAGCAAGGCTCTGCTCTGAC 1289
1091 AACCAGCAACACCGGCGGGGCTGGGGGGCGGCGGCTGCTGCTGCGCGCAGGCTGAGCA 1150
1290 AACCAGCAACACCGGCGGGGCTGGGGGGCGGCGGCTGCTGCTGCGCGCAGGCTGAGCA 1349
1151 CTGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1210
1350 CTGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1409
1211 GTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1270
1410 GTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1469
1271 GCCCGGGCCCAACCGGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1321
1470 GCCCGGGCCCAACCGGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1529
1322 GCCCAAGCCCACTTGGGATGATTAATA 1349
1530 GCCCAAGCCCACTTGGGATGATTAATA 1557

RESULT 3
US-09-661-753-28
Sequence 28, Application US/09661753
Patent No. 6436909
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
FILE REFERENCE: ISPH-0498
CURRENT FILING DATE: 2000-09-14
EARLIER FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 28

LENGTH: 2745
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (842)...(2017)
US-09-661-753-28

Query Match 71.0%; Score 965.8; DB 4; Length 2745;
Best Local Similarity 84.6%; Pred. No. 9.9e-196;
Matches 1146; Conservative 0; Mismatches 147; Indels 62; Gaps 3;

6 CCGAGATGGCGCTTTCGGGCGCTGCGGCTCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 65
837 CCGCATCGCGCTTTCGGGCGCTGCGGCTCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 896
66 TAGTCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 125
897 TGTGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 956
126 AGCTGTGAAGCGGAGGAGCATGAGGAGCATGAGGAGCATGAGGAGCATGAGGAGCATGAGG 185
957 AGCTGTGAAGCGGAGGAGCATGAGGAGCATGAGGAGCATGAGGAGCATGAGGAGCATGAGG 1016
186 TTGCGAGCCCGCGAGCGCAGGAGGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 245
1017 TCGCAGCCCGCGAGCGCAGGAGGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1076
246 CTTCTTACAAAGTACCGCGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 305
1077 CCGTGTACAAAGTACCGCGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1136
306 CAGAGCGGAGTACTACGCGCAAGGAGTACCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 365
1137 CTGAGGCGCGAGTACTACGCGCAAGGAGTACCGCGGCTGCTGCTGCTGCTGCTGCTGCT 1196
366 AATCTATGATTAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 425
1197 AATCTATGATTAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1256
426 AGCTGTGAAGCGGAGGAGCATGAGGAGCATGAGGAGCATGAGGAGCATGAGGAGCATGAG 483
1257 AGCTGTGAAGCGGAGGAGCATGAGGAGCATGAGGAGCATGAGGAGCATGAGGAGCATGAG 1316
484 -GAGGCTCAAGTTAAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 542
1317 GAGGCTCAAGTTAAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1376
543 CTTGCGGCTACCTGAGCAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
1377 CTTGCGGCTACCTGAGCAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1436
603 TTGATGTACACGAGGAGTGTGGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 662
1437 TTGATGTACACGAGGAGTGTGGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 722
663 GCTCTAGTGGCCACTCTTCTCTGACAGCAAGATTAACACTCCACGTCCAGTGGAAATTAAC 722
1497 GCTCTAGTGGCCACTCTTCTCTGACAGCAAGATTAACACTCCACGTCCAGTGGAAATTAAC 1556
723 GGTTCATTTTGGGCGCGCGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 782
1557 GGTTCATTTTGGGCGCGCGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1616
783 TGTCTCATGAGGAGCCCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 842
1617 TGTCTCATGAGGAGCCCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1676
843 GAGCGCTGATTAACCAAGGAGTACCATGAGAGTGCACAGTACCATGCTGCTGCTGCTG 902
1677 GA-----GCCCTGG 1685
903 ATACCACTACTGCTTACGCTTCCACGAGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTG 962

OY	1028	CTGGGGCCCTGTCCCTCAACTCCTGAGACACTGATACAGCAAGGCTCTGGGCTCTG	1087
OY	1236	CTGGGGCCCTGTCCCTCAACTTTTGGAGCTTGGAGACGACGATACAGCAAGGCTCTGGGCTCTG	1295
OY	1088	TACAAACACAGACACAAACCCGGGGCGGCTGTGGCGGGCCCGCTGTCTGGCTGGCGGACGGCGCTGGAG	1147
Db	1296	TACAAACACACATAAACCCGGGGCGGCTGTGGCGGGCCCGCTGTCTGGCTGGCGGACGGCGCTGGAG	1355
OY	1148	CCACAGGCCATCGTGTACTACATCGTGGGGCGGACGCCCAAGGTGGAGAGAGCTGTCCAAATG	1207
Db	1356	CCGCTGCCATCGTGTACTACATCGTGGGGCGGACGCCCAAGGTGGAGAGAGCTGTCCAAATG	1415
OY	1208	ATCGTGTCTTCTCTGCAAGTGCAGCTGAGGCCCGCCCGCCACAGCCCGCCCAACCCGG	1267
Db	1416	ATCGTGTCTTCTCTGCAAGTGCAGCACTGAGGTGCCGCCCCCGCCCGCCCGCCCGCCGACGGC	1475
OY	1268	CAGGCGCGGGCCCAACCCCGCCGCGCT-----CACCGGGGCTGTATTAAAGACA-T	1318
Db	1476	CGGGGCCCAACCGCGCCCGCCGCGCTGTGCCCATGGGGGGTGTATTAAAGACACC	1535
OY	1319	CGTGCCCAAGCCCACTGGGATGATTAATA	1349
Db	1536	CGTGCCCAAGCCCACTGGGCGCCCAATTAA	1566

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RESULT 6
US-09-661-753-1
; Sequence 1, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPh-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 1
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (868)...(2040)
US-09-661-753-1

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Query Match	62.28;	Score 847;	DB 4;	Length 2094;
Best Local Similarity	80.88;	Pred. No. 1.2e-170;		
Matches 1038; Conservative	0;	Mismatches 190;	Indels 57;	Gaps 2

[illegible]

Db	1163	CCGAAGCGGACTACTATATGCTTAAGAAGGTCAACCGGCTGTGTAATATGTGTGAGACCCGACAACG	1222
Qy	366	AAATCTATGATTAATTCAGAGGCAACCCCAACAGCTTATATATATGTGTTCAACAGCTGG	425
Db	1223	CCATCTATAGAGAAACCAAGACATCTCACACAGTATATATATGTTCTTCAATACGTCAG	1282
Qy	426	AGCTCCGGGAACGGGTCGGGAACCTGTAATTTGCTCATCTCGGAGAGAGTCCGGCTGCTGA	485
Db	1283	ACATTCCGGAAACAGTGGCCCGAACCCTCCCATTTGCTGTCCCTGAGAGAGCTGCGCTGGAGA	1342
Qy	486	GGCTCAAGTTAAAAATGTGAGACACAGCTGGAGCTATACAGAAATATACGAATGATTTCT	545
Db	1343	GATTAAAAACAAGTGTGGAGCAACAATGTGMACTCTACCGAAATATAGCAACAATTTCT	1402
Qy	546	GGCGCTACCTCGACAAACCGGCTCGTGCGCCCAAGTGCAGTCTACCGGAGTGGCTGTCCCTTG	605
Db	1403	GGCGTTACCTTGGTAAACCGGCTCTCAACCCCACTGATACCGCTGAATGGCTGTCTTTTG	1462
Qy	606	ATGTCAACCGGAGTTGTGTCGGGCACTGGCTGACCCGACAGAGAGGCTATAGAGGGTTTGGCC	665
Db	1463	ACGTCACTGGAGTTGTAAGGCAAGTGGCTGTAACCAAGAGACGGAAATACAGGGCTTTTGAT	1522
Qy	666	TCAGTGCACCACTCTTCTCTTGACAGAGAAAGATTAACACACTTCACAGTGTGAATTAACGGGT	725
Db	1523	TCAGGCGCTCACTGCTTTGTGACAGAGAAATATACAACATCTCACGTGGAATCAACGGGA	1582
Qy	726	TCAAATCTTGCGCGCCGGGCTGACCTCGGCCACCAATYCACGSGCATAGAACCGGCCCTTCTGTC	785
Db	1583	TCAGCCCCCAACACTGGGGGGGAGACTTGGGACATCATGACATGAAACCGGGCCTTCTCTGC	1642
Qy	786	TCCTCATGCGCCACCCCGCTGTGAGAGAGGCCACAGCACTGCACAGCTCCCGGACCCGCGAG	845
Db	1643	TCCTCATGCGCCACCCCGCTGTGAGAAAGGGCCCGACAGCACTGCACAGCTCACGGCACCCGAGAG	1701
Qy	846	CCCTGGATACCAACAGCTACCCATACGAGAGTGGCAGACTACGCACTCTCTGCGCCCTGGATA	905
Db	1702	-----GCCCTGGATA	1711
Qy	906	CCAACTACTGCTTACAGCTCCACGAGAGAAAGACTGTGCGGACAGCTTACTACTTACT	965
Db	1712	CCAACTATTGCTTACAGCTCCACAGAAAGAAACTGTGTGTGCGGACAGCTTACTACTTACT	1771
Qy	966	TCCGGAAGAACCTGGGGCTGGAATGGAATTCATTAACCCAGAGGGCTACCAATGCCAATTCT	1025
Db	1772	TTAGGAGAGAACCTGGGGTGTGMAATGTGATCCACGACGCCAAGGGCTACCAATGCCAATTCT	1831
Qy	1026	GCCTGGGGGCGCTTCCCTCACTATGTGAGCCTTAAGACACTGATACAGCAAGTCCCTGCTC	1085
Db	1832	GTCTGGGACCTTCCCTCTATTTTGGAGCCTTGAGACACACAGTATACGAAAGTCTCTTGCC	1891
Qy	1086	TGTACACAGCACAAACCGGGGCGCTGGCGGGCGCCGTGCTGTGCTGTCGCGAGGCGCTGG	1145
Db	1892	TCTTACCAACCAACACACCGGGGCGCTTCCGCTGTCACACGTCGTCGTCGCGAGGCTTTGG	1951
Qy	1146	AGCGACTGCCATCGTGTACTACTGTGGGGCGCAAGCCCAAGTGTGAGACAGTGTGCCAACA	1205
Db	1952	AGCGACTGCCATCGTGTACTACTGTGGGTGCAAGCCCAAGTGTGAGACAGTGTGCCAACA	2011
Qy	1206	TGATCTGGTGTCTCTCAAGTGTGAGCTGAGAGGCCCGGCCCGCCACAGCCCGGCCACACC	1265
Db	2012	TGATGTGTGGCTCTCTCAAGTGTGAGCTGAGAGGCCCGGCCCGGCCCGCCCGCTTCC	2065
Qy	1266	GGCAGGCCGGGCCCAACCCCGGCC	1290
Db	2066	GGCAGGCCGGGCCCGGCCCGGCC	2090

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RESULT 7
US-09-661-753-27
; Sequence 27, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:

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QY	186	TTGCGAGCCCCCGGAGCCAGGGGGAGCGTGGCGCCCGCCGCGCTCCGAGCACTACTG	245
Db	436	TCGCCAGCCCCCGGAGCCAGGGGGAGGTGCGCCCGCCGCGCTCCGAGCGCTGCTCG	495
QY	246	CTCTTACACAGTACCGCGCAGCCGGGTAGCCGGGGAAAGTGTGAAACGGAGCCGAGC	305
Db	496	CCCTGTACACAGCACCCCGCGAGCCGGGTGGCCGGGGAGACGGCGGAGCCGAGCCCGAC	555
QY	306	CAGAGGGGAGCTACTACGCGCAAGGAGGTACCCCGCGCTCAATGCTGGAAAGCGGCAAC	365
Db	556	CGGAGCGGAGCTACTACGCGCAAGGAGGTACCCCGCGCTCAATGCTGGAAAGCGGCAAC	615
QY	366	AAATCTATGATAAATTCAGAGGGCACCACCACAGCTTATATGCTTTCACACAGCTCGG	425
Db	616	AAATCTATGACAAAGTTCAAGGAGAGCACACAGCATATATATGTTCTTCAACACATCAG	675
QY	426	AGCTCCGGGAGACGGTGGCCGGAACCTGTATGTCTCTCGGGCAGAGACTGCGCTGCTGA	485
Db	676	AGCTCCGGAGACAGTACCTGGAACCTGTGTGTCTTCCCGGAGAGACTGCGTGTGCGA	735
QY	486	GACCTCAAGTTAAAGTGTGAGCAGCAGCTGAGCTTATACAGAAATACAGCAATGATTCCT	545
Db	736	GCGTCAAGTTAAAGGTGGAGCAGCAGTGTGAGCTGTATCCAGAAATACAGCAACATTCCT	795
QY	546	GAGCGTACCTCAGCAACCGGCTGTGGCCCCCAGTACATCACCGAGTGGCTGTCTTTG	605
Db	796	GAGCGTACCTCAGCAACCGGCTGTGGCCCCCAGCAACTGCGGAGTGGTGTCTTTTG	855
QY	606	ATGTACCGGAGGTTGTGGCGCAGTGGCTACCCGCGAGAGAGCTATATGAGGTTTGGCC	665
Db	856	ATGTACCGGAGGTTGTGGCGCAGTGGTTAGCCGCGAGGGGAAATGAGGGCTTTGGCC	915
QY	666	TCAGTGGCCACCTCTCTCTGTGACAGCAAGATATACACACTCCACGTTGGAATTACGGGT	725
Db	916	TTAGGGCCACAGTCTCTCTGTGACAGCAAGATATACACACTCGCAAGTGCATCAACGGGT	975
QY	726	TCGAATTCGGCCCGCGGGGTGACCTGACCCTTTACGCGCATGAAACGGGCCCTTCTGTC	785
Db	976	TCACACTCGGCGCGCGGAGGTGACCTGGCCACAATTATGCAATGAAGCCGCGCTTCTGTC	1035
QY	786	TCCTCATGCGCACCCCGGCTGGAGAGGGCCAGACCTGACACACTCCCGGACACGCGAG	845
Db	1036	TTTCATGTCGCCACCCCACTGGAGAGGGCCCAACATGTGCAAAAGTCCCGGACCGCGGA	1094
QY	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTAGCATCTCTGGCCCTGATTA	905
Db	1095	-----GCTTTGGATC-----GCTTTGGATC-----	1104
QY	906	CCAACCTACTGCTTCAGCTCCACGGAGAAAGACTGCTGGCGGACGCTCTACTATTGCT	965
Db	1105	CGGCTATTGCTTTTGAAGATGTGACACATTAATGTGTGCTTACGCTCCACTTTACTTATTT	1164
QY	966	TCGCGAAGGACCTGGGCTGGAAGTGGATTCAATGAACCAAGGGCTACCATGCCAATTTCT	1025
Db	1165	TCAGAGGAGGATCTAGGGTGGAAATGATACAGAACCCAAAGGGTACATATGCCAATTTCT	1224
QY	1026	GCTCTGGGGCCCTGTCCCTACACTCTGAGGCTTAGACACTAGTACAGCAAGTCTGTGCTC	1085
Db	1225	GTGCTGGAGCAATGCCCCGATTTATTTATGAGTTCAGACACTAGCAGCAGCAAGGCTGTGAGCT	1284
QY	1086	TGTACAAACAGACAAACCGGGCGGTCGGCGGGCGCGTCTGCTGTCGTCGACGAGCGCTGG	1145
Db	1285	TATATTAATACCAATAATCCAGAGCATCTGCTTCTCTTGTCTGCTGTGCCAGATTTAG	1344
QY	1146	AGCCACTGCCCATGCTGTATCTACGTGGGCGGCAAGGCCCAAGGTGAGCAGCTGTCCACA	1205
Db	1345	AACCTCAACCATCTCTACTACATTTGGCAAAACACCCAAAGATTGAACAGCTTTCTATATA	1404
QY	1206	TGATCTGCGGTTTCTCGCAAGTGCAGCTGA	1234
Db	1405	TGATGTAAAGCTTTCGCAAAATCAGCTAA	1433

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      9  RESULT# 9
      29  US-08-470-837-29
      29  Sequence 29, Application US/08470837
      11  Patent No. 3600811
      11  GENERAL INFORMATION:
      11  APPLICANT: Nimni, Marcel E.
      11  APPLICANT: Hall, Frederick L.
      11  APPLICANT: Tuan, Tai-Lan
      11  APPLICANT: Wu, Lingtao
      11  APPLICANT: Cheung, David T.
      11  TITLE OF INVENTION: Transforming Growth Factor B Fusion
      11  TITLE OF INVENTION: and
      11  TITLE OF INVENTION: Their Use in Wound Healing
      11  NUMBER OF SEQUENCES: 34
      11  CORRESPONDENCE ADDRESS:
      11  ADDRESSEE: Merchant & Gould
      11  STREET: 11150 Santa Monica Boulevard, Suite 400
      11  CITY: Los Angeles
      11  STATE: California
      11  COUNTRY: USA
      11  ZIP: 90025-3395
      11  COMPUTER READABLE FORM:
      11  MEDIUM TYPE: Floppy disk
      11  COMPUTER: IBM PC compatible
      11  OPERATING SYSTEM: PC-DOS/MS-DOS
      11  SOFTWARE: Patentln Release #1.0, Version #1.30
      11  CURRENT APPLICATION DATA:
      11  APPLICATION NUMBER: US/08/470,837
      11  FILING DATE:
      11  CLASSIFICATION: 424
      11  ATTORNEY/AGENT INFORMATION:
      11  NAME: Sharp, Janice A.
      11  REGISTRATION NUMBER: 34,051
      11  REFERENCE/DOCKET NUMBER: 30630-1US01
      11  TELECOMMUNICATION INFORMATION:
      11  TELEPHONE: 310-445-1140
      11  TELEFAX: 310-445-9031
      11  INFORMATION FOR SEQ ID NO: 29:
      11  SEQUENCE CHARACTERISTICS:
      11  LENGTH: 339 base pairs
      11  TYPE: nucleic acid
      11  STRANDEDNESS: double
      11  TOPOLOGY: linear
      11  MOLECULE TYPE: cDNA
      11  FEATURE:
      11  NAME/KEY: CDS
      11  LOCATION: 1..333
      11  FEATURE:
      11  NAME/KEY: CDS
      11  LOCATION: 1..336
      11  FEATURE:
      11  NAME/KEY: mat_peptide
      11  LOCATION: 1
      11  US-08-470-837-29
      11  Query Match 22.8%; Score 310.2; DB 1; Length 339;
      11  Best Local Similarity 94.7%; Pred.No.2,9e-57;
      11  Matches 321; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
      11  QY 896 GCCCTGGATACCACTACTGCTTCAGCTCCACGAGGAAGAACTGCTGCGCGACGCTC 955
      11  DB 1 GCCCTGGAGACCAACTATTGCTTCAGCTCCACGAGGAAGAACTGCTGCGCGACGCTG 60
      11  QY 956 TACATTGACTTCGGGAAGAGACTGGGCTGGGAAGTGGATTTCATGAACCCCAAGGGCTACAT 1015
      11  DB 61 TACATTGACTTCGGGAAGAGACTGGGCTGGGAAGTGGATTTCATGAACCCCAAGGGCTACAT 120
      11  QY 1016 GCCAATTTCTGCGCTGGGGCCCTGTCTCCTACATCTGGAGAGCTAGACACTCAGTACGACGAAG 1075
      11  DB 121 GCCAATTTCTGCGCTGGGGCCCTGTCTCCTACATCTGGAGAGCTCAGTACGACGACGAAG 180
      11  QY 1076 GTCTGGGCTGTGTACACACGACACACCCGGGGCGGCTGGCGGGCGGCTGCTGGCTGCGG 1135
      11  |||||||

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Db 181 GTCTGCGCCCTGTACAAACGACATACCCGGCGCCCTGCGCGCGCCGTGCTGCGTCCG 240
QY 1136 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCGCCGCAAGCCCAAGGTGGAGCAG 1195
|||||
Db 241 CAGGCGCTGGAGCCGCGTCCCATCGTGTACTACGTGGGCGCCGCAAGCCCAAGGTGGAGCAG 300
QY 1196 CTGTCCACATGATGTGCTGCTTCTCTGCAAGTGCAGCTGA 1234
|||||
Db 301 CTGTCCACATGATGTGCTGCTTCTCTGCAAGTGCAGCTGA 339

RESULT 10
US-08-486-057B-1
Sequence 1, Application US/08486057B
Patent No. 5650494
GENERAL INFORMATION:
APPLICANT: Cerletti, Nico
APPLICANT: McMaster, Gary K.
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5650494ak
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005

COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,057B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: No. 5650494ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-17861/+Cont3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..339
FEATURE:
NAME/KEY: CDS
LOCATION: 1..339
US-08-486-057B-1

Query Match 22.7%; Score 308.6; DB 1; Length 339;
Best Local Similarity 94.4%; Pred. No. 6..4e-57;
Matches 320; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 896 GCCCTGATACCACTACTGCTTCAGCTCCAGGAGAAAGACTGCTGCTGGCGGACTC 955
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Db 1 GCCCTGAGACCACTATTGCTTCAGCTCCAGGAGAAAGACTGCTGCTGGCGGACTC 60
QY 956 TACATGACTTCGGAAGGACCTGGGCTGGAAGTATGATGACCAAGGCTTACCAT 1015
|||||
Db 61 TACATGACTTCGGAAGGACCTGGGCTGGAAGTATGATGACCAAGGCTTACCAT 120
QY 1016 GCCAATTTGCTGGGCGCCCTGCTCCCTACATCTGAGCCCTAGACACTGATACGCAAG 1075
|||||
Db 121 GCCAATTTGCTGGGCGCCCTGCTCCCTACATCTGAGCCCTGAGACAGTATACGCAAG 180
QY 1076 GTCTGCTGCTGTACAAACGACACAAACCGGCGCGTGGCGGCGGCTGCTGCTGCCG 1135
|||||
Db 181 GTCTGCGCCCTGTACAAACGACATACCCGGCGCCCTGCGCGGCGGCTGCTGCTGCCG 240
QY 1136 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCGCCGCAAGCCCAAGGTGGAGCAG 1195
|||||
Db 241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCGCCGCAAGCCCAAGGTGGAGCAG 300
QY 1196 CTGTCCACATGATGTGCTGCTTCTCTGCAAGTGCAGCTGA 1234
|||||
Db 301 CTGTCCACATGATGTGCTGCTTCTCTGCAAGTGCAGCTGA 339

RESULT 11
US-08-789-588-1
Sequence 1, Application US/08789588
Patent No. 5922846
GENERAL INFORMATION:
APPLICANT: Cerletti, Nico
APPLICANT: McMaster, Gary K.
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5922846ak
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005

COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,588
FILING DATE:
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989

```
ATTORNEY/AGENT INFORMATION:
NAME: No. 5922846ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-11861+/cont3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..339
FEATURE:
NAME/KEY: CDS
LOCATION: 1..339
US-08-789-588-1
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Query Match 22.7%; Score 308.6; DB 2; Length 339;

Best Local Similarity 94.4%; Pred. No. 6.4e-57;

Matches 320; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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896 GCCCTGGATACCACTACTGCTTCAGCTCCACGAGAGAACGCTGCGTGGCAGCTC 955
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1  GCCCTGGACACCACTATTGCTTCAGCTCCACGAGAGAACGCTGCGTGGCAGCTG 60
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956 TACATTGACTTCCGGAAGACCTGGGCTGGAAAGTGTTCATGACCCAAAGGCTTACC 1015
      |||||||
61 TACATTGACTTCCGGAAGACCTGGGCTGGAAAGTGTTCATGACCCAAAGGCTTACC 120
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1016 GCCAATTTCCTGCTGGGCGCTGCTCCATCTGGAGCTGAGCACTAGTACAGCAAG 1075
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121 GCCAATTTCCTGCTGGGCGCTGCTCCATCTGGAGCTGAGCACTAGTACAGCAAG 180
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1076 GTCTGTGCTGTGTACAAACACACACCGGCGGCTGCGGCGGCGCTGCTGCTGCG 1135
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181 GTCTGTGCGCTGTGTACAAACACACCGGCGGCTGCGGCGGCGCTGCTGCTGCG 240
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1136 CAGCGCGTGGAGCCACTGCTCCATCTGTACTACGTGGGCGGCAAGCCCAAGGTGAGCAG 1195
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241 CAGCGCGTGGAGCCACTGCTCCATCTGTACTACGTGGGCGGCAAGCCCAAGGTGAGCAG 300
      |||||||
1196 CTGTCCAACATGATGCTGCTGCTCCGCAAGTGACGCTGA 1234
      |||||||
301 CTGTCCAACATGATGCTGCTGCTCCGCAAGTGACGCTGA 339
      |||||||
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RESULT 12

US-09-123-233-1

Sequence 1, Application US/09123233

Patent No. 6057430

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: NO. 6057430el process for the production of

TITLE OF INVENTION: biologically active dimeric protein

NUMBER OF SEQUENCES: 14

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/123,233

FILING DATE:

CLASSIFICATION: 530

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 339 base pairs

TYPE: nucleic acid

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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEITICAL: NO
IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLmu.hTGF-beta1 (DSM 5656)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
OTHER INFORMATION: /product= "human TGF-beta1"
US-09-123-233-1
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Query Match 22.7%; Score 308.6; DB 3; Length 339;

Best Local Similarity 94.4%; Pred. No. 6.4e-57;

Matches 320; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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896 GCCCTGGATACCACTACTGCTTCAGCTCCACGAGAGAACGCTGCGGCGCAGCTC 955
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1  GCCCTGGACACCACTATTGCTTCAGCTCCACGAGAGAACGCTGCGGCGCAGCTG 60
      |||||||
956 TACATTGACTTCCGGAAGACCTGGGCTGGAAAGTGTTCATGACCCAAAGGCTTACC 1015
      |||||||
61 TACATTGACTTCCGGAAGACCTGGGCTGGAAAGTGTTCATGACCCAAAGGCTTACC 120
      |||||||
1016 GCCAATTTCCTGCTGGGCGCTGCTCCATCTGGAGCTGAGCACTAGTACAGCAAG 1075
      |||||||
121 GCCAATTTCCTGCTGGGCGCTGCTCCATCTGGAGCTGAGCACTAGTACAGCAAG 180
      |||||||
1076 GTCTGTGCTGTGTACAAACACACCGGCGGCTGCGGCGGCGCTGCTGCTGCG 1135
      |||||||
181 GTCTGTGCGCTGTGTACAAACACACCGGCGGCTGCGGCGGCGCTGCTGCTGCG 240
      |||||||
1136 CAGCGCGTGGAGCCACTGCTCCATCTGTACTACGTGGGCGGCAAGCCCAAGGTGAGCAG 1195
      |||||||
241 CAGCGCGTGGAGCCACTGCTCCATCTGTACTACGTGGGCGGCAAGCCCAAGGTGAGCAG 300
      |||||||
1196 CTGTCCAACATGATGCTGCTGCTCCGCAAGTGACGCTGA 1234
      |||||||
301 CTGTCCAACATGATGCTGCTGCTCCGCAAGTGACGCTGA 339
      |||||||
```

RESULT 13

US-08-868-452-29

Sequence 29, Application US/08868452C

Patent No. 6352972

GENERAL INFORMATION:

APPLICANT: Marcel E. Nimni

APPLICANT: Frederick L. Hall

APPLICANT: Lingtao Wu

APPLICANT: Edwin Shors

TITLE OF INVENTION: BONE MORPHOGENETIC PROTEINS AND THEIR

TITLE OF INVENTION: USE IN BONE GROWTH

FILE REFERENCE: 17972-11

CURRENT APPLICATION NUMBER: US/08/868,452C

CURRENT FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 29

LENGTH: 337

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(336)

US-08-868-452-29

Query Match 22.6%; Score 308.2; DB 4; Length 337;

Best Local Similarity 94.7%; Pred. No. 7.7e-57;

Matches 319; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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896 GCCCTGGATACCACTACTGCTTCAGCTCCACGAGAGAACGCTGCGTGGCAGCTC 955
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1  GCCCTGGACACCACTATTGCTTCAGCTCCACGAGAGAACGCTGCGTGGCAGCTG 60
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Db 1 GCCCTGACACCACTATTGCTTCACTCCAGCGAGAACACTGCTGCGGACGCTG 60
QY 956 TACATTCGATTCGCGAGAGACCTGGCTGGAAGTGGATTCATGAACCCAGGCTACAT 1015
Db 61 TACATTCGATTCGCGAGAGACCTGGCTGGAAGTGGATTCATGAACCCAGGCTACAT 120
QY 1016 GCCAATTTCTGCTGGGCGCTGCTCCCTACATCTGAGGCTAGACACTGATCAGCAG 1075
Db 121 GCCAATTTCTGCTGGGCGCTGCTCCCTACATCTGAGGCTAGACACTGATCAGCAG 180
QY 1076 GTCCGGCTGTACACAGACACACCGGCGCTGGGCGCGCGCTGCTGCTGCGCG 1135
Db 181 GTCCGGCTGTACACAGACACACCGGCGCTGGGCGCGCGCTGCTGCTGCGCG 240
QY 1136 CAGGCGCTGAGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1195
Db 241 CAGGCGCTGAGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 1196 CTGTCACACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1232
Db 301 CTGTCACACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 337

RESULT 14
5168051-9
: Patent No. 5168051
: APPLICANT: DERBYNCK, RIK M.A.; SOEDEL, DAVID V.
: TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
: NUMBER OF SEQUENCES: 21
: CURRENT APPLICATION DATA:
: FILING DATE: 04-AUG-1989
: SEQ ID NO.: 9
: LENGTH: 2671
: 5168051-9

Query Match 18.2% Score 248; DB 6; Length 2671;
Best Local Similarity 52.2%; Pred. No. 5.7e-44;
Matches 653; Conservative 0; Mismatches 555; Indels 42; Gaps 3;

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Db 743 CCAAGCGACCGAGAGAGATGAGTCTTCCAGATCTCCAGCCGATGAGCATATG 802
QY 540 ATTCTGGCGCTACCTGACGACACCGGCTGCTGCGCCCGAGTACTACCGAGTGT 599
Db 803 CCAAGCGACCGAGAGATGAGTCTTCCAGATCTCCAGCCGATGAGCATATG 862
QY 600 CCTTGATGTCACCGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 659
Db 863 CCTTGATGTCACCGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 922
QY 660 TTGCGCTGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGG 719
Db 923 TGAATATCAGATTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 982
QY 720 ACGGCTCAATTCCTGCGCGCGCGGCTGACCTGCGCACCATTGACGCTGACG 779
Db 983 ACATTCAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1042
QY 780 TCTGCTGCTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 839
Db 1043 GTGAGAGCTGCGGCGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1102
QY 840 GCCGAGCGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 899
Db 1103 TGATTCCTCCAGACCGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1162
QY 900 TGGATACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 959
Db 1163 TGGATACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1222
QY 960 TTGACTTCGCGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1019
Db 1223 TTGACTTCGCGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1282
QY 1020 ATTTCGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079
Db 1283 ACTTCGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1342
QY 1080 TGGCTGCTGACACACGACGACACCGGCGGCTGCGGCGGCTGCGGCGGCTG 1139
Db 1343 TGGGCTGCTGACACACGACGACACCGGCGGCTGCGGCGGCTGCGGCGGCTG 1402
QY 1140 CGCTGAGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1199
Db 1403 ACGTGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1462
QY 1200 CCAACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1249
Db 1463 CTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1512

RESULT 15
PCT-US91-04541-1
: Sequence 1, Application PC/TUS9104541
: GENERAL INFORMATION:
: APPLICANT: Oncogene Science Inc.
: TITLE OF INVENTION: TISSUE DERIVED TUMOR GROWTH INHIBITORS
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham
: STREET: 30 Rockefeller Plaza
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10112
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US91/04541

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QY	6	CCGAGATGGGCGCCTTGGGGGCTTCGGGCTTTGGCGCTGCTGGCGGCTGGCTGGGCTGC	65
Db	837	CCCCATCGCGCCCTCCGGGCTCGGCTCGTGGCGCTGTGCTACCGGCTGGCTGTGGCTAC	896
QY	66	TAGGCTGGACGGCTGGCGCGCGCGCGCGGAGCTGTCCACGTGCAAGACCATCGACATGG	125
Db	897	TGGTGTGACCGCTGGCGCGCGCGCGGAGCTATCCACCTGCAAGACTATCGACATGG	956
QY	126	AGCTGTGTAAGCGGAAGCGCATCGAGGCCATTGGCGGCGAGATTCTGTCCAAAGCTTGGGC	185
Db	957	AGCTGTGTAAGCGGAAGCGCATCGAGGCCATTGGCGGCGAGATTCTGTCCAAAGCTTGGGC	1018

QY	186	TTGCCAGCCCCCGGAGCCAGGSGGAGAGTGCCTCCGCGGCCGCTGCTGTGAGGACAGTACTGG	245
Db	1017	TTCCGACGCCCCCGGAGCCAGGSGGAGAGTGCCTCCGCGGCCGCTGCTGTGAGGACAGTACTGG	1076
QY	246	CTCTTTACAAAGTACCCCGGAGCCGGGTAGCCGGGGGAAAGTGTGCAACCGGAGCCGAGC	305
Db	1077	CCCTGTACAAAGTACCCCGGAGCCGGGTAGCCGGGGGAAAGTGTGCAACCGGAGCCGAGC	1136
QY	306	CAGAGCGGAGTACTACGCGCAAGGAGGTACCCGCGTGTAAATGTGGAAAGCGGCAACC	365
Db	1137	CTGAGGCGGAGTACTACGCGCAAGGAGGTACCCGCGTGTAAATGTGGAAAGCGGCAACC	1196
QY	366	AAATCTATATATAATTCAAGGGCACCACCCACAGCTTATATATGCTGTTCACACGTCGG	425
Db	1197	AAATCTATATATAATTCAAGGGCACCACCCACAGCTTATATATGCTGTTCACACATCTAG	1256
QY	426	AGCTCGGGGAGGGGGTGGCGGAACTGTATGTCTCTGCGGGAGAGTGCCTGCTGCT--	483
Db	1257	AGCTCGGAGAGGCGTACTGAAACCCGTGTGTCTCTCCGGCGAGAGCTGCTGTCTGTGA	1316
QY	484	-GAGGCTCAAGTTAAAAAGTGAGAGCAGCGTGAGGCTATACAGAAATACAGCAATGATT	542
Db	1317	GGAGGCTCAAGTTAAAAAGTGAGAGCAGCAGCTGAGGCTATACAGAAATACAGCAATTT	1376
QY	543	CCTGGCGCTACTCAGACAAACCGGCTGCTGGCCCCAGTACTACCGGAGTGGCTGTCTCT	602
Db	1377	CCCTGGGATACCTCAGACAAACCGGCTGCTGGCCCCAGTACTACCGGAGTGGTACTCTT	1436
QY	603	TTGATGTACCCGGAGTTGTAGCGGAGGCGTGCACCGCAAGAGAGGCTATAGAGGTTTTC	662
Db	1437	TTGATGTACCCGGAGTTGTAGCGGAGGCGTGCACCGCAAGAGGGAATTGAGGCGTTTC	1496
QY	663	GGCTCAGTSCCACACTTCTCTCTGACAGCAAGATATAACACATCTCCACGTTGAAATTAAG	722
Db	1497	GCCTTAGCCCCACTCTCTCTGTGACAGCAGGAGTATAACACATCTGAGATCAACG	1556
QY	723	GGTTCATTTCTGGCGCCCGGGGGTGAAGCTGGCCACATTCACGGCATGAAACCGGCTTCC	782
Db	1557	GGTTCCTACTACCGGCGCCCGGAGGTGACCTGGCCACATTCATGGCATATGAACCGGCTTTC	1616
QY	783	TGCTCTCATGCGCACCCGCGCTGGAGAGGGCCAGCACTGCACAGTCTCCGGACCGCC	842
Db	1617	TGCTTCTCATGCGCACCCGCGCTGGAGAGGGCCAGCATCTGCAAAAGTCCCGGACCGCC	1676
QY	843	GAGCCCTGGATACCAACAGCTACCACTACGACGCTGCCAGACTACGATCTGTGGCCCTGG	902
Db	1677	GA-----GCCCCGG	1685
QY	903	ATACCAACTACTGCTTCACTCCACGSGAAGAACTGCTGCTGCGGCACTCTACATTG	962
Db	1686	ACCAACAATTTGCTTCACTCCACGSGAAGAACTGCTGCTGCGGCACTCTACATTG	1745
QY	963	ACTTCGGGAAGGACTGGGGGTGAAGTGTATGTAACCAAGGGCTTACATGCCAATT	1022
Db	1746	ACTTCCGCAAGGACTTGGCTGGAGTGTATCCACGAGGCCCAAGGGCTTACATGCCAATT	1805
QY	1023	TCTGCTGGGGCCCTGTCCCTACATCTGAGACCTTAGACACTACAGCAAGGCTCTGG	1082
Db	1806	TCTGCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACAGCATAGCAAGGCTCTGG	1865
QY	1083	CTTGTGTACAACAGACACACCCGGGGCGTGGCGGGCGCTGTCTGTGCTGCCAGGCGC	1142
Db	1866	CCCTGTACAACAGACATTAACCCGGGGCGCTTGGCGGGCGCTGTGCTGCCAGGCGC	1925
QY	1143	TGGAGGACAGTGGCCATCTGTACTAGTGGGGCGCAAGCCCAAGGTGGAGCAGTGTCCA	1202
Db	1926	TGGAGGCGGCTGCTGTACTAGTGGGGCGCAAGCCCAAGGTGGAGCAGTGTCCA	1985
QY	1203	ACATGATCGTGGCTTCTCTGCAATGACGTGAGGGCCCGGCCCGCCACAGCCGCGCCA	1262
Db	1986	ACATGATCGTGGCTCTCTGCAATGACGTGAGGTCCCGGCCCGGCCCGCCCGCCCGG	2045
QY	1263	CCCGGAGGCGCGCCCGCCACCCCGCGCGCT-----CACCGGGGTGTATTTAAG	1314

Db	2046	CAGGCCGGGGCCACACCCCGCCCCCGCTGCTTGCCTATGGGAGCTATTTAAGG	2105
Qy	1315	ACATCGTGCCTCCCAAGCCCACTTGGAGTGAATTA	1349
Db	2106	ACACGCTGCCCAAGCCCACTGGGGGCCCAATTAA	2140

RESULT 2
US-09-948-002-1
; Sequence 1, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 1
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (868)...(2040)
US-09-948-002-1

Query Match 62.2%; Score 847; DB %: Length 2094;
Best Local Similarity 80.8%; Pred. No. 2,2e-219;
Matches 1038; Conservative 0; Mismatches 199; Indels 57; Gaps

Qy	6	CCGAGATGAGCGCTTCGGGGGCTCGGGCTCTTGGCGCTGCTGCTGCCGCTGCTGGCTGC	65
Db	863	CCCCCATCGCCGCTCGGGGGCTCGGGCTACTGCGCTTCTGCTCCACTCCCGCTGGCTTTC	922
Qy	66	TAGTCTGAGCGCTGGCGCGCGCGCGCGGAGCTGTCCACCTGCAAGACCATCGACATGG	125
Db	923	TAGTCTGAGCGCGCGCGGAGCGCGCGGAGCTGTCCACCTGCAAGACCATCGACATGG	982
Qy	126	AGCTGTGAGGAGGAGGAGCATCGAGGCACTTGGCGGAGATTTGTCGAAGCTTGGCG	185
Db	983	AGCTGTGAGGAGGAGGAGCATCGAGGCACTTGGCGGAGATTTGTCGAAGCTTGGCG	1042
Qy	186	TTGCCAGCCCCCGGAGCCAGGGGAGCTGCCCGCGCGCGCTGCTGAGCGATCTGG	245
Db	1043	TGCCAGTCCCGGAGCCAGGGGAGGATACCGCCCGCGCGCTGCTGAGCGGCTGG	1102
Qy	246	CTCTTTACACAGTATACCGCGGAGCGGGTATAGCGGGGAAAGTGTCCAAACCGAGCCCGAGC	305
Db	1103	CTTTTATACACAGCACCAGCGGAGGAGTACCGCGGCTATGTGGGAAAGCGGCAAC	1162
Qy	306	CAGAGCGGAGCTACTACGCGCAAGAGGTACCGCGGCTATGTGGGAAAGCGGCAAC	365
Db	1163	CCGAGCGGAGCTACTATGCTAAAGAGGTACCGCGGCTATGTGGGAAAGCGGCAACMG	1222
Qy	366	AAATCTATGATTAATTCGAAGGGGACCCCGACAGCTTATATATATGTGTTCAACAGCTCGG	425
Db	1223	CCATCTATGAGAAACCAAGACATCTCACACAGATATATATGTGTTCTTACATAGCTAG	1282
Qy	426	AGCTCCGGGAGAGCGGTGCCGGAACCTGTATTTCTCTCTCGGGCAAGAGCTGGCGCTGCTGA	485
Db	1283	ACATTCGGGAAACAGTGGCCGGAACCCCATTTGCTTCCCGTCCAGAGCTGCCCTTGACA	1342
Qy	486	GGCTCCAGTAAATGAGGAGCAGCGGTGGAGCTTATACAGAAATATACAGATGATTCCT	545
Db	1343	GATTAATAATCAAGTGGGAGCACTGTGGAACTCTACACAGAAATATATACAAATTCCT	1402

QY	546	GGCGTACTCTGACGAACGGGCTGCGGCCAGTACTACCTACCGGAGTGGCTTCCTTG	605
Db	1403	GGCGTTACTCTTGGTAACGGGCTGTGACCCCACTGATATAGCCTGTAGTGGCTCTCTTTTG	1462
QY	606	ATGTCACCCGGAGTTGTGGCGCAGTGGCTGACCOCGACGAGAGGCTATAGAGGTTTCGCC	665
Db	1463	ACGTACAGTGGAGTTGTACGGCAGTGGCTGAACCAAGGAGCGGAATATACAGGGCTTTCGAT	1522
QY	666	TCAGTGGCCACTCTTCCTCTGTGACAGCAAAAGATATACACTCCACGCTGGAAATTAACGGGT	725
Db	1523	TCACGCTCACTGCTCTTCTGTGTGACACCAAAAGATATACAACTCCACGTGGAAATACGGGA	1582
QY	726	TCAATTCGTGGCGCGGGGTGACCTGTGGCCACCATTCACGGCATGAAACCGGCCCTTCCTGC	785
Db	1583	TCAGGCCCAAAAGTGGGGCGACCTGTGGACCATTCATGATATGAACCGGCCCTTCCTGC	1642
QY	786	TCCTCATGGCCACCCCGCTGTGAGAGGGCCAGCAGCTGCACAGCTCCCGGACCGCCGAG	845
Db	1643	TCCTCATGGCCACCCCGCTGTGAGAGGGCCAGCAGCTGCACAGCTGCACGCGCACCGGAGA	1701
QY	846	CCCTGGATACCAACAGTATCCCATATAGAGTGGCAGACTATACGATCTCTGGCCCTGGATA	905
Db	1702	-----GCCCTGGATA 1711	
QY	906	CCAACTACTGCTTTCAGCTTCACGAGAGAAAGTGTGCTGTGCGGACAGCTCTACATTTGACT	965
Db	1712	CCAACTATTGCTTTCAGCTTCACAGAGAAAGTGTGCTGTGCGGACAGCTCTACATTTGACT	1771
QY	966	TCCGAAGAGCTGGGGCTGGAGTGGATTATGAAACCCAAAGGCTACATGCCAATTTCT	1025
Db	1772	TTAGGAAGAGCTGGGGCTGGAGTGGATTATGAAACCCAAAGGCTACATGCCAATTTCT	1831
QY	1026	GCTTGGGGCCCTGTGCTCTACATCTGTGAGGCTGTAGACACTAGTATACAGCAAGTCTGTGCTC	1085
Db	1832	GCTTGGGAACCTGTGCGCCCTATATTTTGGAGCTGTGACACACAGTATACAGCAAGTCTGTGCTC	1891
QY	1086	TGTACACACAGCACAACCCGGGCGCTGGCGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG	1145
Db	1892	TCTACACACCAACACAACCCGGGCGCTTTCGGCGTACACGTGTGCTGTGCTGTGCTGTGCTGTG	1951
QY	1146	AGCCACTGGCCCTGTGCTGTACTAGTGTGGCGGCAAGGCCAAAGGTGGAGCACTGTGCAACA	1205
Db	1952	AGCCACTGGCCCTGTGCTGTACTAGTGTGGCTGTGCAAGGCCAAAGGTGGAGCACTGTGCAACA	2011
QY	1206	TGATGTGCTGTCTGTGCAAGTCAAGCTGAAGCCCGCCGCCACAGCCGCCGCCGCC	1265
Db	2012	TGATGTGCTGTCTGTGCAAGTCAAGCTGAAGCCCGCCGCCACCGCCGCCGCCGCCGCCGCC	2065
QY	1266	GGCAGGCCCGCGGCCACCCCGGCC	1290
Db	2066	GGCAGGCCCGCGGCCCGCCGCCGCC	2090
RESULT 3			
US-09-948-002-27			
: Sequence 27, Application US/09948002			
: Publication No. US20030050265A1			
: GENERAL INFORMATION:			
: APPLICANT: Nicholas M. Dean			
: APPLICANT: Susan F. Murley			
: TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH			
: FILE REFERENCE: ISPH-0607			
: CURRENT APPLICATION NUMBER: US/09/948,002			
: CURRENT FILING DATE: 2000-09-05			
: PRIOR APPLICATION NUMBER: 09/661,753			
: PRIOR FILING DATE: 2000-09-14			
: PRIOR APPLICATION NUMBER: 60/154,546			
: PRIOR FILING DATE: 1999-09-17			
: NUMBER OF SEQ ID NOS: 71			
: SEQ ID NO 27			
: LENGTH: 1585			

[illegible]

Db 1257 CCAACTACTGCTTCCAGTCCACAGAGAAGAACTGCTGTGTACGGCAGCTGTACATTGACT 1316
QY 966 TCCGGAAGAGACTGGGCTGGAAGTATTCATGAACCCAAAGGGCTACCATGCCAATTCT 1025
Db 1317 TTAGGAAGAGACTGGGCTGGAAGTATTCATGAACCCAAAGGGCTACCATGCCAATTCT 1376
QY 1026 GCGTGGGGCCCTGTCCCTACATCTGAGAGCTAGACACTGAGTCAAGAGTCTGTGCTC 1085
Db 1377 GTCTGGGGCCCTGTCCCTACATCTGAGAGCTAGACACTGAGTCAAGAGTCTGTGCTC 1436
QY 1086 TGTATCAACCAAGCAACACCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1145
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QY 1146 AGCCACTGCTCCATGCTGTACTACTGTGGGCGCCAGCCCAAGGAGTGAAGCTGTCCACA 1205
Db 1497 AGCCACTGCTCCATGCTGTACTACTGTGGGCGCCAGCCCAAGGAGTGAAGCTGTCCACA 1556
QY 1206 TGATGTCGCTTCTCTGCAAGTGCAGCTGA 1234
Db 1557 TGATGTCGCTTCTCTGCAAGTGCAGCTGA 1585

RESULT 4

US-09-756-283A-19
; Sequence 19, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
; APPLICANT: Chernaiovsky, Yuli
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Adams, Gillian
; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFERENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LAP-miFbeta construct
; NAME/KEY: CDS
; LOCATION: (1)..(1368)
US-09-756-283A-19

Query Match 48.1%; Score 654; DB 10; Length 1376;
Best Local Similarity 88.1%; Pred. No. 2.9e-167;
Matches 724; Conservative 0; Mismatches 95; Indels 3; Gaps 1;

QY 11 ATGCGCCTTCGCGGGCTGCGGCTCTTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 70
Db 1 ATGCGCCTTCGCGGGCTGCGGCTCTTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
QY 71 CTGACGCTTGGCGCGCGCGCGCGCGGACTGTCACCTGCAAGACCATGACATGAGAGCTG 130
Db 61 CTGACGCTTGGCGCGCGCGCGCGGACTGTCACCTGCAAGACCATGACATGAGAGCTG 120
QY 131 GTGAAGGGAAGGCGCATCGAGGCGCATTTGGCGGCGCATTTCTTCCAAAGCTTGCGCTTGGC 190
Db 121 GTGAAGGGAAGGCGCATCGAGGCGCATTTGGCGGCGCATTTCTTCCAAAGCTTGCGCTTGGC 180
QY 191 AGCCCGCCGAGCCAGGGGAGTGCAGCGCCGCGCGCTGCTGAGAGCAGTACTGGCTCTT 250
Db 181 AGCCCGCCGAGCCAGGGGAGTGCAGCGCCGCGCGCTGCTGAGAGCAGTACTGGCTCTT 240
QY 251 TACAACAGTACCCGCGACCGGGGTAGCCGGGAAAGTGTGCAACCGGAGCCGAGCCAGAG 310
Db 241 TACAACAGTACCCGCGACCGGGGTAGCCGGGAAAGTGTGCAACCGGAGCCGAGCCAGAG 300
QY 311 GCGGACTACTACGCGCAAGAGAGTCAACCCGGGTGCTAATGTGTGGAAGCGGCAACAAT 370
Db 311 GCGGACTACTACGCGCAAGAGAGTCAACCCGGGTGCTAATGTGTGGAAGCGGCAACAAT 370

Db 301 GCCGACTACTAGCCCAAGAGAGTCAACCCGGGTGCTAATGTGTGGAAGCCACACAGGAAT 360
QY 371 TATGATTAATTTCAAGGGGACACCCCGACAGCTTATATGTGTGTTCAACAGCTGGAGCTC 430
Db 361 TATGATTAATTTCAAGGGGACACCCCGACAGCTTATATGTGTGTTCAACAGCTGGAGCTC 420
QY 431 CGGGAAGCGGTGCCGGAAGACCTGTATTGCTCTTCGCGGAGAGAGTGCAGCTGCT--GAGG 487
Db 421 CGAAGAGCGGTGACTGACACCCGCTGTGCTCTCCGCGGAGAGCTGCGCTGCTGAGAGG 480
QY 488 CTCAGTTAAAGTGGAGCAGCAGCTGGAGCTATACAGAAATACAGATGATTCCTGG 547
Db 481 CTCAGTTAAAGTGGAGCAGCAGCTGGAGCTATACAGAAATACAGATGATTCCTGG 540
QY 548 GCTACCTACGACCAACCGGCTGCTGGGCCCCAGTACCTACCGGAGTGGCTGCTTGTAT 607
Db 541 GCTACCTACGACCAACCGGCTGCTGGGCCCCAGTACCTACCGGAGTGGCTGCTTGTAT 600
QY 608 GTACCCGAGATTGTGCGGCAAGTGTGACCCGCGAGAGAGGCTATAGAGGTTTTCGCTC 667
Db 601 GTACCCGAGATTGTGCGGCAAGTGTGACCCGCGAGAGGCTATAGAGGTTTTCGCTC 660
QY 668 AGTCCCACTCTTCTCTGACAGCAAAAGATACACACTCCACGTGGAATTAACGGGTTG 727
Db 661 AGTCCCACTCTCTCTGACAGCAAAAGATACACACTCCACGTGGAATTAACGGGTTG 720
QY 728 AATTCGCGCGCGGGGGTACCTGCGCACCATTCACGAGCATGAACCGGCTTCTGCTC 787
Db 721 AATTCGCGCGCGGGGGTACCTGCGCACCATTCACGAGCATGAACCGGCTTCTGCTC 780
QY 788 CTCATGGCCACCCCGCTGAGAGAGGGCCACAGCACTGCACAGC 829
Db 781 CTCATGGCCACCCCGCTGAGAGAGGGCCACAGCACTGCACAGC 822

RESULT 5

US-09-756-283A-21
; Sequence 21, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
; APPLICANT: Chernaiovsky, Yuli
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Adams, Gillian
; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFERENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 1352
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: miFbeta-LAP construct
; NAME/KEY: CDS
; LOCATION: (1)..(1344)
US-09-756-283A-21

Query Match 43.5%; Score 591.4; DB 10; Length 1352;
Best Local Similarity 87.0%; Pred. No. 2.4e-150;
Matches 662; Conservative 0; Mismatches 96; Indels 3; Gaps 1;

QY 73 GAGCGCTGCGCGCGCGCGCGGACTGTTCACCTGCAAGACCATGACATGAGAGTGGT 132
Db 582 GAGCGGAGGGGCTTACGCGCGCGCACTATCCATGCAAGACTATGACATGAGAGTGGT 641
QY 133 GAAGCGGAAGCCCATCGAGGCGCATTCGCGGCGCGAGATTCTGTCCAAAGCTTGCGCTGCGAG 192
Db 642 GAAGCGGAAGCCCATCGAGGCGCATTCGCGGCGCGAGATTCTGTCCAAAGCTTGCGCTGCGAG 701
QY 193 CCCCCGAGCCAGGGGAGAGTGCAGCGCGCGCGCTGCTGAGAGCAGTACTGGCTCTTTA 252
Db 193 CCCCCGAGCCAGGGGAGAGTGCAGCGCGCGCGCTGCTGAGAGCAGTACTGGCTCTTTA 252

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Db 702 CCCCCGAGCCAGGGGAGGTGCCGCCGCCGCTGCCAGGCGGTGCTGCCCTGTA 761
QY 253 CAACAGTACCCGCGACCGGGTAGCCGGGAGAAAGTGTGAACCGGAGCCGAGCAGAGGC 312
Db 762 CAACAGCACCACCGGACCGGGTGGCGGGAGAGTGCAGAACCGGAGCCGAGCCTGAGGC 821
QY 313 GGACTACTACGCCAGAGAGGTCAACCCGCTGAATGATGGAAGAGCGGCAACCAATGTA 372
Db 822 CGACTACTAGCCAGAGAGGTCAACCCGCTGAATGATGGAAGAGCGGCAACCAATGTA 881
QY 373 TGATTAATTCAGAGGCAACCCGCAACACTTATATATGCTGTTCACAGCTGGAGCTCG 432
Db 882 TGCAAGTTCAAGAGTACACACACATATATATGTTCTTCAACATCAGAGCTCG 941
QY 433 GGAAGCGGTGCCGGAACCTGTATGCTCTCGGGCAGAGCTGGCGCTGCT---GAGGCT 489
Db 942 AGAAGAGGTACCTGAACCCGCTGTGCTCTCCGGGAGAGCTGCTGCTGAGAGAGCT 1001
QY 490 CAAGTTAAAGTGGAGCAGACGCTGAGCTATACAGAAATACAGCAATGATTCCTGCG 549
Db 1002 CAAGTTAAAGTGGAGCAGACGCTGAGCTATACAGAAATACAGCAATGATTCCTGCG 1061
QY 550 CTACTCAGAACCGGCTGTGCTGCCGCCAGTGAAGCTCAGCGAGTGGCTGCTTGTAGT 609
Db 1062 ATACCTCAGAACCGGCTGTGCTGCCGCCAGTGAAGCTCAGCGAGTGGCTGCTTGTAGT 1121
QY 610 CACCGAGTGTGCGGAGTGTGCTGACCCGAGAGAGCTATAGAGGTTTTCGCTCAG 669
Db 1122 CACCGAGTGTGCGGAGTGTGCTGACCCGAGAGAGCTATAGAGGTTTTCGCTCAG 1181
QY 670 TGGCCACTCTTCTCTGACAGCAAAATTAACACACTCCAGCTGGAATTAAGGGTTCAA 729
Db 1182 TGGCCACTCTTCTCTGACAGCAAAATTAACACACTCCAGCTGGAATTAAGGGTTCAA 1241
QY 730 TTTGCGCCCGCGGGGAGCTGCGCCACATTCACGGCATGACCGGCTTCCGCTGCT 789
Db 1242 TACCGCGCCCGGAGGTGACTGCGCCACATTCATGCGCATGACCGGCTTCCGCTGCT 1301
QY 790 CATGGCCACCCCGCTGGAGAGGGGCCAGACGCTGCACAGCT 830
Db 1302 CATGGCCACCCCGCTGGAGAGGGGCCAGACGCTGCACAGCT 1342

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RESULT 6

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US-09-813-271B-1
; Sequence 1, Application US/09813271B
; Patent No. US20020115834A1
; GENERAL INFORMATION:

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APPLICANT:
TITLE OF INVENTION: (A) NICO Cerletti
biologically active protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: No. US20020115834A1artis Patent Department
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,271B
FILING DATE: 20-Mar-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02719
FILING DATE: 12-Jul-95
APPLICATION NUMBER: EPO 94810439.3
FILING DATE: 25-Jul-94

```

```

ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hessa, J.
REGISTRATION NUMBER: 22640
REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522-5940
TELEFAX: (908) 522-6955
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLMu.hTGF-beta1 (DSM 5656)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
OTHER INFORMATION: /product= "human TGF-beta1"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-813-271B-1

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Query Match 22.7% Score 308.6; DB 10; Length 339;
Best Local Similarity 94.4%; Pred. No. 4.7e-74;
Matches 320; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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QY 896 GCCCTGATACCACTACTGCTTACGCTCCAGGAGAGAACTGTGCTGCGGACGCTC 955
Db 1 GCCCTGAGACCAACTATTGCTTACGCTCCAGGAGAACTGTGCTGCGGACGCTC 60
QY 956 TACATTGACTTCCGGAAGACCTGGGCTGGAAGTGGATTGATGATACCAAGGCTTACAT 1015
Db 61 TACATTGACTTCCGGAAGACCTGGGCTGGAAGTGGATTGATGATACCAAGGCTTACAT 120
QY 1016 GCCAATTTCTGCTGGGCGCTGCTCCCTACATCTGGAGCTTAGACATCAGTACAGCAAG 1075
Db 121 GCCAATTTCTGCTGGGCGCTGCTCCCTACATCTGGAGCTTAGACATCAGTACAGCAAG 180
QY 1076 GTCCGTGGCTCTGACACAGCAGAACCCGGGCGCTCGGCGGCGCGTGTGCTGCTGCG 1135
Db 181 GTCCGTGGCTCTGACACAGCAGAACCCGGGCGCTCGGCGGCGCGTGTGCTGCTGCG 240
QY 1136 CAGGCGCTGAGCCACTGCCATCGTACTACAGTGGGCGGCAAGCCCAAGGTGGAGCAG 1195
Db 241 CAGGCGCTGAGCCACTGCCATCGTACTACAGTGGGCGGCAAGCCCAAGGTGGAGCAG 300
QY 1196 CTGTCCACATGATGCTGCTGCTGCAAGTGCAGCTGA 1234
Db 301 CTGTCCACATGATGCTGCTGCTGCAAGTGCAGCTGA 339

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RESULT 7

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US-10-028-158-20
; Sequence 20, Application US/10028158
; Patent No. US20020110833A1
; GENERAL INFORMATION:
APPLICANT: Caniglia, Isabella
APPLICANT: Post, Martin
TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
TROPIC BLAST
FILE REFERENCE: 1175.38USWO
CURRENT APPLICATION NUMBER: US/10/028,158
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US/09/380,662
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: PCT/CA98/00180
PRIOR FILING DATE: 1998-03-05
PRIOR APPLICATION NUMBER: US 60/039,919
PRIOR FILING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 24

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Db      301 CTTTCTAATATGATTTGTAAGTCTTGCAATGCAGC 336

RESULT 11
US-09-813-271B-9
; Sequence 9, Application US/09813271B
; Patent No. US20020115834A1
; GENERAL INFORMATION:
; APPLICANT:
; (A) NICO Cerletti
; TITLE OF INVENTION: New process for the production of
; biologically active protein
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. US20020115834A1artis Patent Department
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,271B
; FILING DATE: 20-Mar-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/02719
; FILING DATE: 12-Jul-95
; APPLICATION NUMBER: EPO 94810439.3
; FILING DATE: 25-Jul-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Pfeiffer, Heena J.
; REGISTRATION NUMBER: 22640
; REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 522-6940
; TELEFAX: (908) 522-6955
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "recombinant hybrid DNA
; IMMEDIATE SOURCE:
; CLONE: E. coli LC137/pPLMu.TGF-beta2(44/45)betas3
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..132
; OTHER INFORMATION: /product= "N-terminal 44 amino
; acids of human TGF-beta2"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 133..336
; OTHER INFORMATION: /product= "C-terminal 68 amino
; acids of human TGF-beta3"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
; OTHER INFORMATION: /product= "hybrid TGF-beta2-3"
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-813-271B-9

Query Match 13.3%, Score 180.8; DB 10; Length 336;
Best Local Similarity 71.1%; Pred. No. 1.6e-39;
Matches 239; Conservative 0; Mismatches 97; Indels 0; Gaps
0;

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biologically active protein

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: No. US20020115834Marti's Patent Department
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,271B
FILING DATE: 20-Mar-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02719
FILING DATE: 12-Jul-95
APPLICATION NUMBER: EPO 94810439.3
FILING DATE: 25-Jul-94
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Henna J.
REGISTRATION NUMBER: 22640
REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522-6940
TELEFAX: (908) 522-6955
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLMu.hTGF-beta2 (DSM5657)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
OTHER INFORMATION: /product="human TGF-beta2"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-813-271B-3

Query Match 11.6% Score 158.2; DB 10; Length 339;
Best Local Similarity 66.7%; Pred. No. 2.1e-33;
Matches 226; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

896 GCCCTGGATGCAACCTACTGCTGCTCCAGAGAGAACTGCTGCGGCGAGCTC 955
1 GCTTTGGATGGGCTATGCTTGAATGTCAGAGAAATGCTGCTGCTGCTCCACTT 60
956 TACATGACTTCCGGAAGACCTGGGCTGGAAGTATTCATGAGACCAAGGCTTACAT 1015
61 TACATGATTTCAAGAGGATCTAGAGGTGAATGATACAGAACCCAAAGGTTACAAAT 120
1016 GCCAATTTCTGCGGCGGCTGTCCTACATCTGAGGCTGAGACCTAGTACAGCAAG 1075
121 GCCCACTTCTGCTGGAGCATGCCGATTTATGAGAGTTTCAGACACTGACGACAGG 180
1076 GTCCGTGCTGTGATACACAGACACCGGCGGCTGCGGCGGCTGCTGCTGCGG 1135
181 GTCTGAGCTTATATAATACATAATCCAGAAAGATCTGCTTCTGCTGCTGCTCC 240
1136 CAGGCGCTGAGACCACTGCGCATGCTGATCTAGTGGGCGGCAAGCCCAAGTGGAGCAG 1195
241 CAAGATTTAGAACCTTACCACTTCTCTACTACATTCGCAAAACACCAAGATTGAACAG 300
1196 CTGTCAACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1234
301 CTTTCTAATATGATTGTAAGTCTTGCAATGACGCTAA 339

RESULT 14
US-10-044-090-323
Sequence 323, Application US/10044090
Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 323
LENGTH: 2912
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 3146342CB1
US-10-044-090-323

Query Match 11.6% Score 158.2; DB 12; Length 2912;
Best Local Similarity 66.7%; Pred. No. 3.4e-33;
Matches 226; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

896 GCCCTGGATGCAACCTACTGCTGCTCCAGAGAGAACTGCTGCGGCGAGCTC 955
1604 GCTTTGGATGGGCTATGCTTGAATGTCAGAGAAATGCTGCTGCTGCTCCACTT 1663
956 TACATGACTTCCGGAAGACCTGGGCTGGAAGTATTCATGAGACCAAGGCTTACAT 1015
1664 TACATGATTTCAAGAGGATCTAGGAGTAATGATACAGAACCCAAAGGTTACAAAT 1723
1016 GCCAATTTCTGCGGCGGCTGTCCTACATCTGAGGCTGAGACCTAGTACAGCAAG 1075
1724 GCCAATTTCTGCTGGAGCATGCCGATTTATGAGAGTTTCAGACACTGACAGCAGG 1783
1076 GTCCGTGCTGTGATACACAGACCAAGCCGCGGCTGCGGCGGCTGCTGCTGCTGCTG 1135
1784 GTCCGTGCTTATATAATACATAATCCAGAAAGATCTGCTTCTGCTGCTGCTGCTC 1843
1136 CAGGCGCTGAGACCACTGCGCATGCTGATCTAGTGGGCGGCAAGCCCAAGTGGAGCAG 1195
1844 CAAGATTTAGAACCTTACCACTTCTCTACTACATTCGCAAAACACCAAGATTGAACAG 1903
1196 CTGTCAACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1234
1904 CTTTCTAATATGATTGTAAGTCTTGCAATGACGCTAA 1942

RESULT 15
US-09-864-761-15319/c
Sequence 15319, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aemica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04

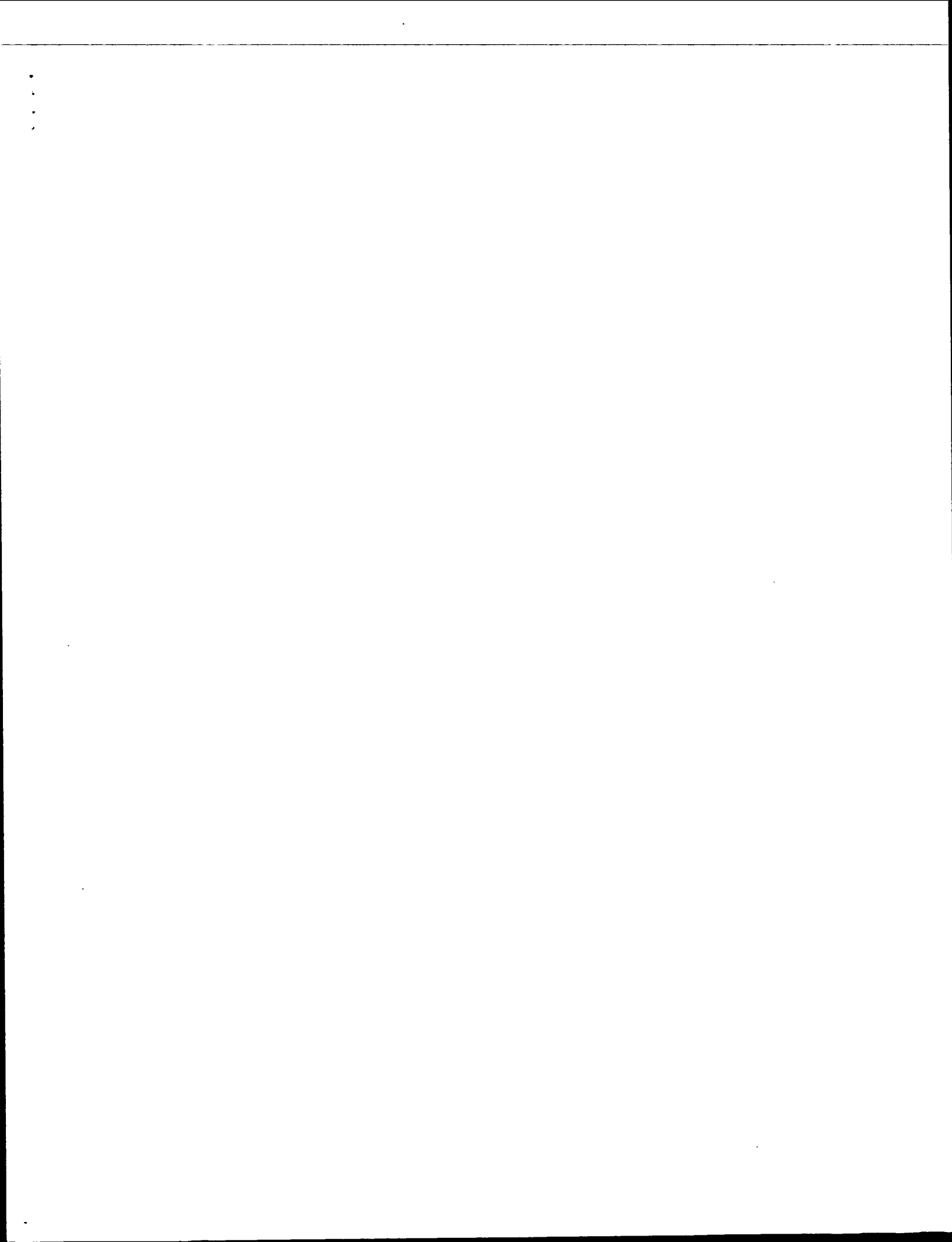

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1  PRIOR APPLICATION NUMBER: US 60/236,359
2  PRIOR FILING DATE: 2000-09-27
3  PRIOR APPLICATION NUMBER: PCT/US01/00666
4  PRIOR FILING DATE: 2001-01-30
5  PRIOR APPLICATION NUMBER: PCT/US01/00667
6  PRIOR FILING DATE: 2001-01-30
7  PRIOR APPLICATION NUMBER: PCT/US01/00664
8  PRIOR FILING DATE: 2001-01-30
9  PRIOR APPLICATION NUMBER: PCT/US01/00669
10 PRIOR FILING DATE: 2001-01-30
11 PRIOR APPLICATION NUMBER: PCT/US01/00665
12 PRIOR FILING DATE: 2001-01-30
13 PRIOR APPLICATION NUMBER: PCT/US01/00668
14 PRIOR FILING DATE: 2001-01-30
15 PRIOR APPLICATION NUMBER: PCT/US01/00663
16 PRIOR FILING DATE: 2001-01-30
17 PRIOR APPLICATION NUMBER: PCT/US01/00662
18 PRIOR FILING DATE: 2001-01-30
19 PRIOR APPLICATION NUMBER: PCT/US01/00661
20 PRIOR FILING DATE: 2001-01-30
21 PRIOR APPLICATION NUMBER: PCT/US01/00670
22 PRIOR FILING DATE: 2001-01-30
23 PRIOR APPLICATION NUMBER: US 60/234,687
24 PRIOR FILING DATE: 2000-09-21
25 PRIOR APPLICATION NUMBER: US 09/608,408
26 PRIOR FILING DATE: 2000-06-30
27 PRIOR APPLICATION NUMBER: US 09/774,203
28 PRIOR FILING DATE: 2001-01-29
29 NUMBER OF SEQ ID NOS: 49117
30 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
31 SEQ ID NO 15319
32 LENGTH: 597
33 TYPE: DNA
34 ORGANISM: Homo sapiens
35 FEATURE:
36 OTHER INFORMATION: MAP TO AC011462.3
37 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9
38 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
39 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5
40 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.8
41 US-09-864 -761-15319

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	Query Match	10.4%	Score 141.6	DB 10	Length 597
	Best Local Similarity	91.5%	Pred. No. 7.3e-29		
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QY	916	CTTACGCTCCACGGAGAAACTGCTGGCTGGCAGCCTACATTGATCTCCGAGGA	975		
Db	458	CTGCAGCTCCACGGAGAAAGTCTGCTGGCAGCTGACATTGATCTCCGAGGA	399		
QY	976	CCTGGGCGGGAAGTGAGATTCAATGAACCCAAAGGCGCTACCATGTCCTGGGGCC	1035		
Db	398	CCTGGGCTGGGAAGTGAGATCCACGAGCCCAAGGGCTACCATGCCAATCTTGCTGGGGCC	339		
QY	1036	CTGTCCCTACATCTGAGACCTAGACACTACATAGCAGAGGTCC	1079		
Db	338	CTGGCCCTACATTTGGAGACCTGAGACACCCAGTACAGCAGGTAC	295		

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Job time : 206 secs



GenCore version 5.1.4-p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 10:09:10 ; Search time 2186 seconds
(without alignments)
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Title: US-10-017-372E-36

Perfect score: 1361

Sequence: 1 cgtacagagatgcgcctt.....cgattaagcgccgcgact 1361

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Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008
Listing first 45 summaries

Database :

EST:*
1: em_estha:*
2: em_esthum:*
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5: em_estov:*
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9: gp_estl:*
10: gp_est2:*
11: gp_hlc:*
12: gp_est3:*
13: gp_est4:*
14: gp_est5:*
15: em_estlin:*
16: em_estom:*
17: gp_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_dln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_nod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	703.6	51.7	1072	13	BM562135
2	607	44.6	1043	13	BM555996
3	577.4	42.4	789	9	AL530081
4	570.6	41.9	713	10	BE312000
5	562.6	41.3	717	10	BE260971
6	562	41.3	902	14	BQ675698

7	534.4	39.3	925	13	BT188841	BT188841	603037307
C	8	521.4	38.3	956	13	BT1884718	BT1884718
C	9	517.6	38.0	798	9	AL530080	AL530080
	10	513.8	37.8	871	14	BQ52138	BQ52138
	11	506.6	37.2	1013	13	BM469326	BM469326
	12	506.6	37.2	1093	14	BM054305	BM054305
	13	504.8	37.1	943	13	BT1909079	BT1909079
	14	502	36.9	821	12	BT6748049	BT6748049
	15	501.8	36.9	773	13	BT195242	BT195242
	16	498.8	36.6	1049	14	BM053417	BM053417
	17	472.8	34.7	675	10	BE261764	BE261764
	18	466.2	34.3	727	9	AT131171	AT131171
	19	461	33.9	785	9	AT148173	AT148173
	20	459.8	33.8	637	13	BM938856	BM938856
	21	455.8	33.5	748	12	BF682938	BF682938
	22	455.4	33.5	814	13	BT686959	BT686959
	23	452.2	33.2	548	13	BM068788	BM068788
	24	450	33.1	982	14	BM072677	BM072677
	25	447.6	32.9	981	14	BM802192	BM802192
	26	446	32.8	659	12	BM500488	BM500488
	27	444.6	32.7	778	9	AT743724	AT743724
	28	443.6	32.6	1015	12	BM683840	BM683840
	29	442.4	32.5	636	10	BE615330	BE615330
	30	441.6	32.4	599	13	BT1905963	BT1905963
	31	435	32.0	821	10	BE311897	BE311897
	32	434.4	31.9	1228	14	BM917472	BM917472
	33	432	31.7	676	14	BM974192	BM974192
	34	426	31.3	660	13	BM251237	BM251237
	35	425.8	31.3	664	9	AL044345	AL044345
	36	425	31.2	662	14	BM576225	BM576225
	37	423.2	31.1	943	14	BM675477	BM675477
	38	421.6	31.0	678	14	BQ021537	BQ021537
	39	418.6	30.8	660	14	BQ018647	BQ018647
	40	416.4	30.6	1028	14	BQ670359	BQ670359
	41	411.8	30.3	540	13	BT1834732	BT1834732
	42	411.4	30.2	719	14	BQ780439	BQ780439
	43	409.6	30.1	654	14	BM681750	BM681750
	44	408.8	30.0	639	12	BF723491	BF723491
	45	406.2	29.8	869	14	BQ879491	BQ879491

ALIGNMENTS

RESULT 1
LOCUS BM562135
DEFINITION AGENCOURT_6562032 NIH_MGC_118 Homo sapiens CDNA clone IMAGE:5745463
ACCESSION BM562135
VERSION BM562135.1 GI:18807966
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1072)
AUTHORS NIH-MGC
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM12768 row: h column: 08
High quality sequence start: 9
High quality sequence stop: 647.
Location/Qualifiers

FEATURES

source		1. 1072	
		/organism="Homo sapiens"	
		/db_xref="taxon:9606"	
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		/issue="NIH_MGC_118"	
		/library="Leukocyte"	
		/lab_host="DH10B"	
		/note="Vector: PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is Oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."	
BASE COUNT		217 a 356 c 313 g 186 t	
ORIGIN			
Query Match		51.7%; Score 703.6; DB 13; Length 1072;	
Best Local Similarity		81.6%; Pred. No. 2.1e-143;	
Matches 886; Conservative		0; Mismatches 144; Indels 56; Gaps 4;	
QY	127	GGTGGTGAAGCGAAGCGATCGAGGCGCATTCGGCGGCAGATTCGCAAGCTTGGCT	186
DB	20	GCTGGTGAAGCGAAGCGATCGAGGCGCATTCGGCGGCAGATTCGCAAGCTTGGCT	79
QY	187	TGCCAGCCCCCGAGCGAGGCGACGTCCGCGCGCGCGCTGCTGAGGCGAGTCTGGC	246
DB	80	CCCCAGCCCCCGAGCGAGGCGAGGCGCGCGCGCGCGCGCGCGCTGCTGAGGCGAGC	139
QY	247	TCTTACACAGTACCGCGGCGAGCGGAGGCGGAGGAGTGTGCAACGCGAGCCGAGCC	306
DB	140	CCTGTACACAGTACCGCGGCGAGCGGAGGCGGAGGAGTGTGCAACGCGAGCCGAGCC	199
QY	307	AGAGCGGCGATCTACGCGCAAGAGGTACCCGCGTGTAAATGTGTGAAGCGGCAACA	366
DB	200	TGAGCGCGGCGATCTACGCGCAAGAGGTACCCGCGTGTAAATGTGTGAAGCGGCAACA	259
QY	367	AATCTGTGAATTAATTAAGGCGGCGCGCGAGCTTATATATGCTGTGTTCAACGCGGCA	426
DB	260	AATCTGTGAATTAATTAAGGCGGCGCGAGCTTATATATGCTGTGTTCAACGCGGCA	319
QY	427	GCTCCGGAAGCGGTGCGGGAACCTGTATTGCTCTCTGCGGCGAGCTGCGCTGTGAG	486
DB	320	GCTCCGGAAGCGGTGCGGGAACCTGTATTGCTCTCTGCGGCGAGCTGCGCTGTGAG	379
QY	487	GCTCAAGTTAAAGTGAAGCGACGCTGAGCTATACAGAAATACAGCAATGATTCCTG	546
DB	380	GCTCAAGTTAAAGTGAAGCGACGCTGAGCTATACAGAAATACAGCAATGATTCCTG	439
QY	547	GCGCTACCTAGCAACGCGGCTGTGCGCGCGAGTACTACCGGAGTGGCTGTCTTTGA	606
DB	440	GCGATACCTAGCAACGCGGCTGTGCGCGCGAGTACTACCGGAGTGGCTGTCTTTGA	499
QY	607	TGTCACCGGAGTGTGCGGCGAGTGGCTGACCGCGAGAGAGGCTATGAGGCTTTGGCT	666
DB	500	TGTCACCGGAGTGTGCGGCGAGTGGCTGACCGCGAGAGAGGCTATGAGGCTTTGGCT	559
QY	667	CAGTGGCCACTCTCTCTGTGACGCAAGATTAACACATCTCCAGTGAATTAACGGGT	726
DB	560	TAGGCGCCACTCTCTCTGTGACGCAAGATTAACACATCTCCAGTGAATTAACGGGT	619
QY	727	CAATCTGAGCGCGGGGTGACCTGCGCACATTCAGCGAGATGAACCGGCGCTTCTGCT	786
DB	620	CACATACCGCGCGCGAGTGTGACCTGCGCACATTCAGCGAGATGAACCGGCGCTTCTGCT	679
QY	787	CCTCATGCGCACCGCGGTGAGAGGCGCGACACTGCAACAGTCCCGGAGCGCGGAGC	846
DB	680	TCTCATGCGCACCGCGGTGAGAGGCGCGACACTGCAACAGTCCCGGAGCGCGGAGC	739
QY	847	CCTGATACCAACAGCTACCCATAGAGAGTGCACAGTCTGCGCCCTGATATAC	906

DB	740	-----CCCTGGACAC	749
QY	907	CAACTACTGCTTACGCTCCACGAGAGAACTGCTGCGGCGAGCTATCTACTGACTT	966
DB	750	CACATATTGCTTACGCTCCCGGAGAGAACTGCTGCGGCGAGCTATCTACTGACTT	809
QY	967	CCGGAAGACCTGGGCTGAGATGATTCATGAACCCAGGGCTACCTATGCAATTTCTG	1026
DB	810	CCGCAAGACCTGGGCTGAGATGATTCATGAACCCAGGGCTACCTATGCAATTTCTG	869
QY	1027	CCGCGGCGCGCTGCGCTTACATCTGAGAGCTGACACTGACAGCGGTACCAAGTCTGCT	1086
DB	870	CCGCGGCGCGCTGCGCTTACATCTGAGAGCTGACACTGACAGCGGTACCAAGTCTGCT	929
QY	1087	GTACACACACACACACACCGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTG	1144
DB	930	GTACACACCGCATATACCGGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTG	989
QY	1145	GAGCCACTGCCCAT--CGTGTACTACGTGGGCGCG--AAAGCCAAAGTGGAGCAGCTGTC	1200
DB	990	GACCCCTGCGCGCTTGGGCGTACTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCTG	1049
QY	1201	CAACAT 1206	
DB	1050	CCACAT 1055	
RESULT 2			
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LOCUS BM555996			
DEFINITION 5', mRNA sequence.			
AGENCOURT_6544437 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5550039			
VERSION BM555996.1 GI:18796907			
KEYWORDS EST.			
SOURCE human.			
ORGANISM Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE 1 (bases 1 to 1043)			
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.			
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL Unpublished (1999)			
COMMENT Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LLM12261 row: 1 column: 16 High quality sequence stop: 702.			
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source			
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/db_xref="taxon:9606"			
/clone="IMAGE:5550039"			
/issue="NIH_MGC_88"			
/lab_host="DH10B (phage-resistant)"			
/note="Organ: small intestine; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."			
BASE COUNT			
202 a 329 c 345 g 154 t 13 others			
ORIGIN			
Query Match 44.6%; Score 607; DB 13; Length 1043;			
Best Local Similarity 80.9%; Pred. No. 2.6e-122;			
Matches 734; Conservative 0; Mismatches 122; Indels 51; Gaps 1;			

QY	396	ACAGCTTATATATGCTGTTCAACACGTGGAGCTCCGGGAGCGGTGCGGACCTGTAT	455
Db	1	ACAGGATATATATGTTCTTCAACACATCAGACTCCGAGAACCGGTAACCTGAT	60
QY	456	TGCTCTCTCGGGCAGAGCGTGGCGCTGCTGAGGCTCAAGTTAAAGTGGAGCAGCAGTGG	515
Db	61	TGCTCTCTCCGGGACAGAGCTGCGTCTGCTGAGGCTCAAGTTAAAGTGGAGCAGCAGTGG	120
QY	516	ACCTATACCAAGAAATACAGCAATGATTCCTGGCGCTACTCAGCAACCGGCTGTGGCCC	575
Db	121	ACCTGTACCAAGAAATACAGCAACATTCCTGGCGATACCTCAGCAACCGGCTGTGGCAC	180
QY	576	CCAGTGAAGTACACCGAGTGGCTGCTCTTGAATGATCAGCGGAGTGTGGCGCAGTGGCTGA	635
Db	181	CCAGGAGCTCCGCAAGTGGTATCTTTTGAATGATCAGCGGAGTGTGGCGCAGTGGTGA	240
QY	636	CCGCGAGAGAGGCTTATAGAGGGTTTTCGCTCAGTGGCCCACTTCCTCTCTGACAGCAAG	695
Db	241	GCCGTGGAGAGGAAATTTGAGGGCTTTTCGCTTATAGCGCCACTGCTCTCTGACAGAGGG	300
QY	696	ATATACACACTCCAGGTGGAATTAACGGGGTTCAATTCCTGGCCCGCGGGGTGACCTGGCCA	755
Db	301	ATATACACACTCCAGAGTGACATCAAGGGTTCACTACAGCGCGCGGAGGTGACCTGGCCA	360
QY	756	CCATTTCAGCGGATGTAACCGGGCCCTCTCTCTCTATGATGCCACCCCGCTGGAGAGGCC	815
Db	361	CCATTTCATGCGATGTAACCGGGCCCTCTCTCTCTATGATGCCACCCCGCTGGAGAGGCC	420
QY	816	AGCAGCTGACAGAGCTCCCGGACGCGCCGAGCCCTGATATCAACAGCTAACCATACGAGC	875
Db	421	AGCATCTGCAAGAGCTCCCGGACGCGCCA-----	449
QY	876	TGCCAGACTAGCATCTCTGGCCCTGGATACCAACTACTGCTTCAGCTCCACGAGAGAGA	935
Db	450	-----GCCCTGGACACCAACTGATTCCTCAGCTCCACGAGAGAGA	489
QY	936	ACTGCTGGCTGGCGGAGCTCTTACATTGACTTCCGAGAGAGCCTGGGCTGGAGTGGATTC	995
Db	490	ACTGCTGGCTGGCGGAGCTCTTACATTGACTTCCGAGAGAGCCTGGGCTGGAGTGGATTC	549
QY	996	ATGAACCCCAAGGGCTACCATGCAATTTCTGCTGGGGCCCTGCTCCCTACATCTGGAAGCC	1055
Db	550	ACGAGCCCAAGGGCTACCATGCAATTTCTGCTGGGGCCCTGCTCCCTACATTTTGAAGCC	609
QY	1056	TAGACACTAGTACAGCAAGGCTGCTCTGTATACACAGCAGCAACCCGGCGGCTGCG	1115
Db	610	TGGACACAGAGTACAGCAAGGCTGCTGCTGTATACACAGCAGTAAACCGGCGGCTGCG	669
QY	1116	CGGGCCGCGGCTGGCGGCGGAGGGGCTGGAGACCACTGCCATTCGTATCTACGTGGGCC	1175
Db	670	CGGGCCGCGGCTGGCGGCGGAGGGGCTGGAGACCACTGCCATTCGTATCTACGTGGGCC	729
QY	1176	GCAAGCCCAAGGTGGAGCAGCTGTCCACATGATGCTGCTCTGCAAGTGAAGTGAAGTGA	1235
Db	730	GCAAGCCCAAGGTGGAGCAGCTGTCCACATGATGCTGCTCTGCAAGTGAAGTGAAGTGA	789
QY	1236	GCCCGCGCCCGCCACAGCCCGCCACCGGCAAGCCCGGCCCAACCCCGCGCGCTC	1295
Db	790	GCGTCCGCGCCCGCCACAGCCCGGCGGCGGCGGCGGCGGCGCGCGCGCGC	849
QY	1296	ACCGGGG 1302	
Db	850	GGCGCGG 856	

RESULT 3

AL530081

LOCUS

DEFINITION

ACCESSION

VERSION

AL530081

AL530081.LTI.NF1001.NBC4

prime mRNA sequence.

AL530081

AL530081.1

789 bp

mRNA

linear

EST 13-FEB-2001

Homo sapiens cDNA clone CS0DD009YK06 5

GI:12793574

KEYWORDS	EST.	human.
SOURCE	ORGANISM	Homo sapiens
REFERENCE 1 (bases 1 to 789)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.		
TITLE Full-length cDNA libraries and normalization		
JOURNAL Unpublished (2001)		
COMMENT Contact: Genoscope		
	Genoscope - Centre National de Sequencage	
	BP 191 91006 EVRY cedex - France	
	Email: seqlife@genoscope.cns.fr , Web : www.genoscope.cns.fr .	
FEATURES	Location/Qualifiers	
source	1..789	
	/organism="Homo sapiens"	
	/db_xref="taxon:3606"	
	/clone="CS0DD009YM06"	
	/clone_lib="LTI_NFL001_NBC4"	
	/sex="male"	
	/tissue_type="neuroblastoma cells"	
	/lab_host="HDH10B"	
	/note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-0.150(5') primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filang@lifestech.com URL : http://fulllength.invitrogen.com "	
BASE COUNT	159 a 254 c 240 g 134 t	2 others
ORIGIN		
Query Match	42.4%	Score 577.4; DB 9; Length 789;
Best Local Similarity	87.0%;	Pred. No. 6.9e-116;
Matches 643: Conservative	2; Mismatches 93; Indels 1; Gaps 1;	
6	CCGAGATGGCGCTTCGGGGGCGCGGCTCTTGCCGCTGCTGGCCGTGGCGTGGCGC	65
11		
51	CCCCATGCGGCCCTTCGGGGCTGCGGGCTGCTGCTCTGCTACCGCTGCTGAGCTAC	110
66	TAGTCTGACGCGCTGGCGCGCGCGCGCGGCACTGTCCACTGCAAGACCATCGACATGG	125
111	TGTTGCTGACGCGCTGGCGCGCGCGCGCGGCACTGTCCACTGCAAGACCATCGACATGG	170
126	AGCTGCTAACGCGAAGGCGCATCGAGGCGCATTTGCGGGCGACATTTGTGTCGAAGCTTGGCC	185
171	AGCTGCTAACGCGAAGGCGCATCGAGGCGCATTTGCGGGCGACATTTGTGTCGAAGCTTGGCC	230
186	TTGGCAGCGCCCCCGAGGCGGAGGCGCGCGCGCGCGCGCGCGCTGCTAGGACAGTACTGG	245
231	TGGCCAGCGCCCCCGAGGCGGAGGCGCGCGCGCGCGCGCGCGCGCTGCTAGGACAGTACTGG	290
246	CTCTTTAAACAAGTACCCCGGCGGCGGCTGAGCGGGGAAAGTGTGCAACCGGACCGGACG	305
291	CCCTGTAAACAAGCACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	350
306	CAGAGCGCGGACTACAGCCCAAGGAGGTGACCCCGGCTGCTATGTTGGTGAAGAAGCGGCAAC	365
351	CTGAGCGCGGACTACTACGCGCAAGGAGGTGACCCCGGCTGCTATGTTGGTGAAGAAGCGGCAAC	410
366	AAATCTATGATTAATTCAGGCGCACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	425
411	AAATCTATGATTAATTCAGGCGCACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	470
426	AGCTCCGGGAGGCGGTGGCGGAGCGTGTATGTTGCTCTGCGGGCGAGAGTGGCGGCTGTGA	485
471	AGCTCCGGGAGGCGGTGGCGGAGCGTGTATGTTGCTCTGCGGGCGAGAGTGGCGGCTGTGA	530
486	GGCTCAAGTTAAAGTGAGGAGGACGCTGGAGGCTATACAGAAATATACGACATGATTCTCT	545

Db 531 GGCTCAAGTTAAAGTGGAGACAGACGTGAGCTGTACAGAAATACAGCAATTCCT 590
 Oy 546 GCGCTACTCTACAGAACCGGCTCTGGCCCCCACTGACTACCCGAGTG -GCTGCTTT 604
 Db 591 GCGGATCTCTACAGAACCGGCTCTGGCCCCCACTGACTACCCGAGTGACTTCTTT 650
 Oy 605 GATGTCACCGGATTTGGGCGAGTGGTACCAGAGAGAGGCTATAGAGGTTTTCG 664
 Db 651 GATGTCACCGGATTTGGGCGAGTGGTACCAGAGAGAGGCTATAGAGGTTTTCG 710
 Oy 665 CTCAGTCCCACTCTCTCTGACAGCAAGATATACACTCTCCAGCTGGAATTAACGG 724
 Db 711 CTAGGCGCCACTGCTCTCTGACAGCAAGATATACACTCTCCAGCTGGAATTAACGG 770
 Oy 725 TTCAATTTGGCGCGCGG 743
 Db 771 TTCTACTACGCGCGCGAG 789

RESULT 4
 BE312000 713 bp mRNA linear EST 26-OCT-2000
 LOCUS 601154768F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3510592 5',
 DEFINITION mRNA sequence.
 ACCESSION BE312000
 VERSION BE312000
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 713)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: L1CM195 row: h column: 17
 High quality sequence start: 2
 High quality sequence stop: 713.
 Location/Qualifiers

FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3510592"
 /clone_lib="NIH_MGC_19"
 /tissue_type="neuroblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; CDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 BASE COUNT 157 a 226 c 211 g 119 t
 ORIGIN

Query Match 41.9%; Score 570.6; DB 10; Length 713;
 Best Local Similarity 87.5%; Pred. No. 2.1e-14;
 Matches 624; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

Oy 135 AGGGAGAGCGATCGAGCGCATTCGCGGAGATTCGCAAGCTTGGCTTGGCCAGCC 194
 Db 1 AGCGGAGAGCGATCGAGCGCATTCGCGGAGATTCGCAAGCTTGGCTTGGCCAGCC 60

Oy 195 CCCCCAGCAGAGGGAGAGTGGCCCCCGGCGCTGCTGAGGAGTACTGCTTTACA 254
 Db 61 CCCCCAGCAGAGGGAGAGTGGCCCCCGGCGCTGCTGAGGAGTACTGCTTTACA 120
 Oy 255 ACAGTACCCCGGAGCGGTACCCGGGGAAGTGTGAACCGGAGCCGAGAGCGG 314
 Db 121 ACAGACCCCGGAGCGGTGCGGGGAGAGTGAAGAACCGGAGCCGAGAGCGG 180
 Oy 315 ACYACTACGCCAAGAGAGTACCCGCGTGTATGTTGTAAGAGGAGGAGCAACAATCTATG 374
 Db 181 ACTACTACGCCAAGAGAGTACCCGCGTGTATGTTGTAAGAGGAGGAGCAACAATCTATG 240
 Oy 375 ATAAATTCAGAGGCAACCCCAACAGTATATATGCTGTTCACACAGTGGAGCTCGGG 434
 Db 241 ACAAGTTCAACGACAGATACACACAGATATATATGTTTTCACACATGAGACTCCGAG 300
 Oy 435 AAGGGTGGCCGAACCTATATGCTCTCGGCGAGAGCTGGCGCTGAGGCTCAAGT 494
 Db 301 AAGGGTGGCCGAACCTATATGCTCTCGGCGAGAGCTGGCGCTGAGGCTCAAGT 360
 Oy 495 TAAAGTGGAGCAGCAGCTGAGCTATACAGAAATACAGCAATGATTCCTGGCGTACC 554
 Db 361 TAAAGTGGAGCAGCAGCTGAGCTATACAGAAATACAGCAATGATTCCTGGCGTACC 420
 Oy 555 TCAGCAACCGGCTGCTGCGCCCCAGTACTACCGGAGTGGCTGTCTTTGATGTACCG 614
 Db 421 TCAGCAACCGGCTGCTGCGCCCCAGTACTACCGGAGTGGTATCTTTGATGTACCG 480
 Oy 615 GAGTTGGCGGAGAGGCTGACCCGAGAGAGGCTATAGAGGTTTGGCTGAGTCCG 674
 Db 481 GAGTTGGCGGAGAGGCTGACCCGAGAGAGGCTATAGAGGTTTGGCTGAGTCCG 540
 Oy 675 ACTTCTCTCTGACAGCAAGATTAACACACTCCAGCTGGAATTAACGGGTTCAATTCG 734
 Db 541 ACTGCTCTCTGACAGCAGAGGATTAACACACTCCAGCTGGAATTAACGGGTTCAATTCG 600
 Oy 735 GCGCGCGGGGAGTACTGGCGCACCATTCACAGGATGAACGGCCCTCTCTCTCAATG 794
 Db 601 GCGCGCGGGGAGTACTGGCGCACCATTCACAGGATGAACGGCCCTCTCTCTCAATG 660
 Oy 795 CCACCCCGCTGGAGAGGCGCCAGCACTGACAGCTCCCGGAGCGCGAGCC 847
 Db 661 CCACCCCGCTGGAGAGGCGCCAGCACTGACAGCTCCCGGAGCGCGAGCC 713

RESULT 5
 BE260971 717 bp mRNA linear EST 26-OCT-2000
 LOCUS 601153715F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509921 5',
 DEFINITION mRNA sequence.
 ACCESSION BE260971
 VERSION BE260971
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 717)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: L1CM193 row: m column: 04
 High quality sequence stop: 713.
 Location/Qualifiers

FEATURES
 Source
 1..717

Query Match 41.9%; Score 570.6; DB 10; Length 713;
 Best Local Similarity 87.5%; Pred. No. 2.1e-14;
 Matches 624; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

Oy 135 AGGGAGAGCGATCGAGCGCATTCGCGGAGATTCGCAAGCTTGGCTTGGCCAGCC 194
 Db 1 AGCGGAGAGCGATCGAGCGCATTCGCGGAGATTCGCAAGCTTGGCTTGGCCAGCC 60

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:350931"
 /clone.lib="NIH_MGC_19"
 /tissue_type="neuroblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: Brain; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(6). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 158 a 226 c 213 g 120 t
 ORIGIN

Query Match 41.3%; Score 562.6; DB 10; Length 717;
 Best Local Similarity 87.4%; Pred. No. 1.2e-112;
 Matches 627; Conservative 0; Mismatches 89; Indels 1; Gaps 1;

136 GCGGAGCCGATCGAGGCCATTCGCGCGCATTCGTCACAGCTTGCGGTGGCAGCCC 195
 1 GCGGAGCCGATCGAGGCCATTCGCGCGCATTCGTCACAGCTTGCGGTGGCAGCCC 60
 196 CCCGAGCCAGGGGAGCGCGCCGCCGCTGCTGAGGCACTACTGCTTTACAA 255
 61 CCCGAGCCAGG-GGAGGTGCGCGCGCGCTGCGCGAGCGCTGCTCGCCCTACAA 119
 256 CAGTACCGCGGCGCGGTGCGCGGGAAGTGTGCAACCGGAGCCGAGGCGCGA 315
 120 CAGCACCGCGGCGCGGTGCGCGGGAAGTGTGCAACCGGAGCGCTGAGCGCA 179
 316 CTACTACGCCAAGAGAGTACCGCGCTGCTAATGTTGGAAGCGGCAACCAATCTATGA 375
 180 CTACTACGCCAAGAGAGTACCGCGCTGCTAATGTTGGAAGCGGCAACCAATCTATGA 239
 376 TAAATTCAGGGGACCCCGACAGCTTATATGCTGTTCAACAGCTGAGATCCGGA 435
 240 CAAATTCAGGGGACCCCGACAGCTTATATGCTGTTCAACAGCTGAGATCCGGA 299
 436 ACCGCTGCGGAGACCTGATGCTCTGCGGCGAGAGCGGCTGCTGAGGCTCAAGTT 495
 300 ACCGCTGCTGAACCCGCTGTTGCTCTCCGCGGAGAGCTGCTGCTGAGGCTCAAGTT 359
 496 AAAAGTGAAGCAGCAGTGAAGTATACCAAGAAATACAGCAATGATTCGCGGCTACT 555
 360 AAAAGTGAAGCAGCAGTGAAGTATACCAAGAAATACAGCAATGATTCGCGGCTACT 419
 556 CAGCAACCGGCTGCTGCGGCGGAGTACTACCGGAGTGGCTCTCTTATGATGTCACGG 615
 420 CAGCAACCGGCTGCTGCGGCGGAGTACTACCGGAGTGGCTCTCTTATGATGTCACGG 479
 616 AGTTGTGGGCGAGTGGCGGCGGAGGCTATAGAGGGTTTGCGGCTCAGTGGCA 675
 480 AGTTGTGGGCGAGTGGCGGCGGAGGCTATAGAGGGTTTGCGGCTCAGTGGCA 539
 676 CTCTTCCTCTGACAGCAAAATPAACACTCACTGGAATTAACGGGTTCAATTTGG 735
 540 CTCTTCCTCTGACAGCAAAATPAACACTCACTGGAATTAACGGGTTCAATTTGG 599
 736 CCGCGGGGAGTGAAGTGAAGCAATTCAGGCAATTCAGGCGCTTCTCTCTCATAGGC 795
 600 CCGCGGGGAGTGAAGTGAAGCAATTCAGGCAATTCAGGCGCTTCTCTCTCATAGGC 659
 796 CACCCGCTGAGAGGGCCAGACCTCCGACAGCTCCGCGACCGGAGCCCTTGA 852
 660 CACCCGCTGAGAGGGCCAGACCTCCGACAGCTCCGCGACCGGAGCCCTTGA 716

RESULT 6
 B0675698 902 bp mRNA linear EST 15-JUL-2002
 LOCUS B0675698

DEFINITION AGENCOURT_8036532 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6211917
 5' mRNA sequence.
 B0675698
 B0675698.1 GI:21786532
 EST.
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 902)
 NIH-MGC http://mgc.ncl.nih.gov/.
 AUTHORS Unpublished (1999)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM2375 row: c column: 22
 High quality sequence stop: 599.
 Location/Qualifiers
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 /clone="IMAGE:6211917"
 /clone.lib="NIH_MGC_102"
 /tissue_type="epidermoid carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: salivary gland; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(6). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 194 a 292 c 255 g 161 t
 ORIGIN

Query Match 41.3%; Score 562; DB 14; Length 902;
 Best Local Similarity 86.7%; Pred. No. 1.7e-112;
 Matches 619; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

156 TTCCGCGCCAGATTCTGTCCAGCTTCGCGGCTTCCAGCCCGGAGCCAGGGGAGCTGC 215
 1 TCCTGCGGCGAGTCTGTCCAGCTTCGCGGCTTCCAGCCCGGAGCCAGGGGAGCTGC 60
 216 GCGCGGCGCGGCTGCTGAGGAGTACTGCTCTTTACAGAGTACCCGCGGAGTATG 275
 61 GCGCGGCGCGGCTGCTGAGGAGTACTGCTCTTTACAGAGTACCCGCGGAGTATG 120
 276 CCGGGAAGTGTGCAACCGGAGCCGAGCCAGAGCGGAGTACTACGCGCAAGAGAGTCA 335
 121 CCGGGAAGTGTGCAACCGGAGCCGAGCCGAGCGGAGTACTACGCGCAAGAGAGTCA 180
 336 CCGCGGCTCTAATGTGTGAAGCGGCAACCAATCTATGATTAATTCAGAGCCACCCCG 395
 181 CCGCGGCTCTAATGTGTGAAGCGGCAACCAATCTATGATTAATTCAGAGCCACCCCG 240
 396 ACAGCTTATATGCTGTTCACACAGCTGCGGAGCTCCGCGGAAACGGTGAACCTGTAT 455
 241 ACAGCTTATATGCTGTTCACACAGCTGCGGAGCTCCGCGGAAACGGTGAACCTGTAT 300
 456 TGTCTCTCGGCGAGAGCTGCGCTGCTGAGGCTCAAGTTAAAGTGAAGCAGCAGCTGG 515
 301 TGTCTCTCGGCGAGAGCTGCGCTGCTGAGGCTCAAGTTAAAGTGAAGCAGCAGCTGG 360
 516 AGCTATCCCAAAATACAGCAATGATTCCTTGGCGCTACTCTAGCAACCGGCTGCGGCC 575

DB	676	TCAGCGCTCAGCTGCTCTGTGTGACAGCAAGAAAGATTAACANAACTCCAGCTGGAATCAACGGN	735
QY	725	TTCAA--TTCTGGCCGGCGGGGTGACCTGGC-CACCATTTCAAGGCATGAA-CCGGCCCT	779
DB	736	GATCAGCCCCCAACGTCGGGGGGCGACCTGGGNGCAGCATTCATGACATGAANACGGCCCT	795
QY	780	TCCTGCTCTCTATGGC--CAGCCCGCTGGAGAGGCCCAAGACCTGG	823
DB	796	TCCTGCTCTCTCATGGCAACCCCCCTGTGAAAGGCCAGCAGCACTGG	841
RESULT 11			
LOCUS	BM469326	1013 bp	mRNA
DEFINITION	AGENCOURT_6480727 NIH_MGC_85 Homo sapiens	linear	EST 05-FEB-2002
ACCESSION	5', mRNA sequence.		
VERSION	BM469326		
KEYWORDS	BM469326.1 GI:18518368		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota, Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;		
TITLE	Mammalia, Eutheria: Primates, Catarrhini, Hominiidae, Homo.		
JOURNAL	1 (bases 1 to 1013)		
COMMENT	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strusberg, Ph.D. Email: rgs@bbs.fmail.nih.gov Tissue Procurement: Lou Staudt cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LNLMI2265 row: f column: 23 High quality sequence stop: 530. Location/Qualifiers 1. 1013 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_image="55151510" /clone_lib="NIH_MGC_85" /tissue_type="lymphoma, cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: lymph; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."		
FEATURES			
source			
BASE COUNT	225 a	333 c	291 g
ORIGIN			163 t 1 others
Query Match	37.2%	Score 506.6;	DB 13; Length 1013;
Best Local Similarity	88.9%;	Pred. No. 2.1e-100;	
Matches 559;	Conservative	0; Mismatches 69;	Indels 1; Gaps 1;
QY	6	CCGAGATGCGCCCTTCGGGCGCTGTCCTTCGCCGTGCTGCCCGCTGTGGCTGC	65
DB	9	CCCCCATGCCGCCCTCGGGCGCTGCTGCTCCCTGCTGTACCGGTGCTGGCTAG	68
QY	66	TAGTGTGACGGCTGGCGCGCGCGCGCGGAGCTGTCCACCTGGAAAGCATGACATG	125
DB	69	TGGTCTGACGCTTGGCGCGCGCGCGCGGAGCTGTCCACCTGCAAGACTATGACATG	128
QY	126	AGCTGTGTAAGCGAAGCGCATGAGCCATTGCGGCGCAGATGCTGTCCAAGCTTCGCG	185
DB	129	AGCTGTGTAAGCGAAGCGCATGAGCCATTGCGGCGCAGATGCTGTCCAAGCTTCGCG	188
QY	186	TTGCGACGCCCCCGAAGCGAGGGGACGTGCGCGCGCGCGCTGCTGTAGGCACTGACTGG	245
DB	189	TGCGACGCCCCCGAAGCGAGGGGACGTGCGCGCGCGCGCTGCTGTAGGCACTGACTGG	248

OY	246	CTCTTTAAACAGTATCCCGCAGC	CGBGGTGATGCGCGGAAGAATGTGTGCAACCGGACCCGAGC	305
Db	249	CCCTTATACAGCACGCCGCAGC	CGBGGTGCGCGGAGAGTCAGAAACC	308
OY	306	CAGAGCGGACTACTACGCCCAAG	GAGGTACACCCGGTGCTTAATG	355
Db	309	CTGAGGCGGACTACTACGCCCAAG	GAGGTACACCCGGTGCTTAATG	368
OY	366	AAATCTATGATAAATTCAAGGG	CACCCCAACAGCTTATATATGCTGTTTAAACAGCTGG	425
Db	369	AAATCTATGACAAGTTCAAGCAG	AGATTACACAACAGCATATATGTTCTTCAACACATCAG	428
OY	426	AGCTCCGGGAGAACGGTGGCCG	AACCTGTATTGTCTCTCGGGCAGAGCTGGCGCTGCTGA	485
Db	429	AGCTCCGGGAGAACGGTGGCTG	TAAACCCGGTGTCTCTCCGGGCAAGAGCTGGCTGTGCTGA	488
OY	486	GGCTCAAGTTAAAATGTGAGCAG	CACGCTGGAGACTATTACAGAAATACAGCAATGATTGCT	545
Db	489	GGCTCAAGTTAAAATGTGAGCAG	CACGCTGGAGACTATTACAGAAATACAGCAATGATTGCT	548
OY	546	GGCGCTACCTCAGCAACCGGCT	GCTGGCCCCCACTGACTACCCGAGTAGGCTGTCTTTG	605
Db	549	GGCGATACCTCAGCAACCGGCT	GCTGGCCCCCACTGACTACCCGAGTAGGCTGTCTTTG	608
OY	606	ATGTACAC-GGAGTTGTGCGGCA	GTGGCT	633
Db	609	ATGTACACCGGAGTTGTGCGGCA	GTGGGT	637
RESULT_12				
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DEFINITION	AGNCOCURT.6830409 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5936397			
ACCESSION	B0054305			
VERSION	B0054305.1		GI:19813645	
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
TITLE	NIH-MGC http://mgc.nci.nih.gov/			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Dr. Daniel McVicar, DBS/NCI CDNA Library Preparation: Rubin Laboratory/ CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: L1CM2125 row: k column: 22 High quality sequence stop: 605. Location/Qualifiers 1..1093 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5936397" /clone_lib="NIH_MGC_106" /tissue_type="natural killer cells, cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: blood; Vector: pOT87; Site:1: XhoI; Site:2: EcoRI; CDNA made by oligo-dT priming, directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGCGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Nih MGC Library." Note: this is a			
FEATURES	source			

BASE COUNT	233 a	347 c	309 g	203 t	1 others
ORIGIN					
Query Match	37.2%; Score 506.6; DB 14; Length 1093;				
Best Local Similarity	82.5%; Pred. No. 2,2e-100;				
Matches 682; Conservative	0; Mismatches 79; Indels 54; Gaps 2;				
QY	535 CAATGATTCCTGGCGGCTACCTGACACACCGGCTGCTGGCCCCAGTACGACTCCAGCGAGTG 594				
DB	1 CAACAATTCCTGGCGGCTACCTGACACACCGGCTGCTGGCCCCAGTACGACTCCAGCGAGTG 60				
QY	595 GGTGCTCTTGGATGTACACCGGAGTGTGTGGCGAGTGGCTGACCCCGAGAGAGGCTATAGA 654				
DB	61 GTTATCTTTTGGATGTACACCGGAGTGTGTGGCGAGTGGCTGACCCCGAGAGAGGCTATAGA 120				
QY	655 GGGTTTCCGCTTACGTAGTCCCACTTCTCTCTGTACAGCAAGAATAACACTCCACGTGCA 714				
DB	121 GGGCTTTTCCGCTTACGTAGTCCCACTTCTCTCTGTACAGCAAGAATAACACTCCACGTGCA 180				
QY	715 AATTAAGGGTTCATTCCTGGCGCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCG 774				
DB	181 CATCAACGGGTTCTACTACCGGCGCGCGGGGTGACCTGGCCACCATTCATGGCATGAACCG 240				
QY	775 GCGCTTCTGCTCTCTCTATGGCCACCGCGCTGAGAGGGCCCAAGCACTGACAGCTCCCG 834				
DB	241 GCGTTTCTGCTCTCTCTATGGCCACCGCGCTGAGAGGGCCCAAGCACTGACAGCTCCCG 300				
QY	835 GCACCGCGCGCGCTGATACCAACAGTACCCATACACAGTGCAGACTAGCATCTCT 894				
DB	301 GCACCGCGCG----- 310				
QY	895 GCGCTGATACCAACTACTGCTTACGCTCCAGCGAGAGAAAGTCTGCTGGCGAGCT 954				
DB	311 -GCGCTGAGACCAACTATGCTTACGCTCCAGCGAGAGAAAGTCTGCTGGCGAGCT 369				
QY	955 CTACATTTGACTTCCGAGAGGAGCTGGGCTGGAAGTGAATTCATGAACCCCAAGGGCTACCA 1014				
DB	370 GTACATTTGACTTCCGAGAGGAGCTGGGCTGGAAGTGAATTCACAGACCCCAAGGGCTACCA 429				
QY	1015 TGGCATTTTGTGCTGGGGGCGCTGCTCCCTACATCTGAGAGCCATAGACACTACAGCAA 1074				
DB	430 TGGCATTTTGTGCTGGGGGCGCTGCTCCCTACATTTGAGAGCCATAGACACTACAGCAA 489				
QY	1075 GGTCTGAGCTCTGTATACACAGACAAACCGGGCGCTGGGGCGCGCTGCTGCTGCC 1134				
DB	490 GGTCTGAGCTCTGTATACACAGACAAACCGGGCGCGCTGCTGCTGCTGCC 549				
QY	1135 GCAGGCGCTGAGGAGCACTGCCATCGTGTACTACGTGGGGCGCGCAAGCCCAAGGTGAGCA 1194				
DB	550 GCAGGCGCTGAGGAGCGCTGCCATCGTGTACTACGTGGGGCGCGCAAGCCCAAGGTGAGCA 609				
QY	1195 GGTGTCCAATATATGCTGGGCTGTCTGCAATGCACTGAGGCGCGCGCGCGCGCGCACG 1254				
DB	610 GGTGTCCAATATATGCTGGGCTGTCTGCAATGCACTGAGGAGG---GTCCGCGCGCGCGCG 666				
QY	1255 CCGGCG 1295				
DB	667 GCCCG 707				
RESULT 13					
LOCUS	BI909079 943 bp mRNA linear EST 16-OCT-2001				
DEFINITION	603070060F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218983 5',				
ACCESSION	BI909079 mRNA sequence.				
VERSION	BI909079.1 GI:16172210				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 943)				

AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHAM11550 row: 9 column: 16 High quality sequence stop: 682.				
FEATURES	location/qualifiers				
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	/clone_1ib="NIH_MGC_118"				
	/tissue_type="leukocyte"				
	/lab_host="DH10B"				
	/note="Vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."				
BASE COUNT	170 a	315 c	291 g	166 t	1 others
ORIGIN					
Query Match	37.1%; Score 504.8; DB 13; Length 943;				
Best Local Similarity	80.4%; Pred. No. 5.2e-100;				
Matches 682; Conservative	0; Mismatches 147; Indels 19; Gaps 7;				
QY	6 CCGAGATGGCGGCTTGGGGGCTGGGCTCTTGGCGGCTGGCTGGCTGGCGCTGGCGCTGC 65				
DB	95 CCGCATGCGGCGCTTGGGGGCTGGGCTCTTGGCGGCTGGCTGGCTGGCGCTGGCGCTGC 154				
QY	66 TAGTGCTAGCGGCTTGGGGGCTGGGCTCTTGGCGGCTGGCTGGCTGGCGCTGGCGCTGC 125				
DB	155 TGGTGCTAGCGGCTTGGGGGCTGGGCTCTTGGCGGCTGGCTGGCTGGCGCTGGCGCTGC 214				
QY	126 AGCTGTGAAGCGGAAGCGCATTCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 185				
DB	215 AGCTGTGAAGCGGAAGCGCATTCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 274				
QY	186 TTGGCAGCGCGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 245				
DB	275 TTGGCAGCGCGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 334				
QY	246 CTCTTTACAGAGTACCGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 305				
DB	335 CCTGTACAGAGGAGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 394				
QY	306 CAGAGGCGGAGTACTAGGCA-AGGAGGTACCGCGGCTGTATGTGGGAAA-GCGGCAA 363				
DB	395 CTGAGCGGAGTACTAGGCAATGAGGAGGTACCGCGGCTGTATGTGGGAAAACCGGACAA 454				
QY	364 CCAATCTATGATTAATTCAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 423				
DB	455 CGAATCTATGATTAATTCAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 514				
QY	424 GGAGCTCCGGGAGGCGGTGCGGAGCCTGTATTTCTCTCGGCGGAGAGGCTGCGCTGCT 483				
DB	515 AGAGCTCCGAGAGGCGGTGCGGAGCCTGTATTTCTCTCGGCGGAGAGGCTGCGCTGCT 574				
QY	484 GAGGCTCAAGTTAAAAGTGAGGAGCAGCTGTAGCTATACCAAGAAATACGAATGATTC 543				
DB	575 GAGGCTCAAGTTAAAAGTGAGGAGCAGCTGTAGCTATACCAAGAAATACGAATGATTC 634				

Query Match	36.98; Score 502; DB 12; Length 821;
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found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM1858 row: c column: 05

FEATURES
source High quality sequence stop: 708.
Location/Qualifiers
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/clone="IMAGE:5092540"
/clone_id="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

Db 719 CGGACCGCGCGCATGGACACACCAATTCG 751
Search completed: April 15, 2003, 11:52:21
Job time : 2239 secs

BASE COUNT 183 a 229 c 230 g 131 t
ORIGIN

Query Match 36.9%; Score 501.8; DB 13; Length 773;
Best Local Similarity 83.5%; Pred. No. 2.2e-99;
Matches 629; Conservative 0; Mismatches 117; Indels 7; Gaps 5;

117 TCGACATGGAGTGTGAAGCGGAGCGCATCGGCATTCGCGCCAGATTCTGTCCA 176
1 TCGACATGGAGTGTGAAGCGGAGCGCATCGGCATTCGCGCCAGATTCTGTCCA 61
177 AGCTTCGGCTTCCAGCCCCCGAGCGGGGAGCTGCCGCCCGCTGCTGAGG 236
62 AGCTCGGGCTCCAGCCCCCGAGCGAGGTGAGGTGCCG-CCGGCCCGCTGCCGAG 120
237 CAGTACTGGCTTTACACAGTACCGCGGAGCGGTAAGCGGGAAGTGTCAACCG 296
121 CCGTCTGCGCTGTACACAGCAGCCCGGAGCGGGTGGCCGGGAGAGTCAAGACCG 180
297 AGCCGAGCAGAGCGGAGCTACTAGCCCAAGAGAGTACCCGCGCTCTAAATGTGAAA 356
181 AGCCGAGCCTGAGCGCGACTACTAGCCCAAGAGAGTACCCGCGCTCTAAATGTGAAA 240
357 GCGGCAACCAATCTATTAATTCAGAGGACCCCGACAGCTTATATATGTGTCA 416
241 CCCACACGAAATCTATTAAGTTCAGAGAGTACACAGCATATATATGTGTCTCA 300
417 ACACGTCGAGTCCCGGAGCGGTGCGGAACTGTATGCTCTCTCGGCGAGCTGC 476
301 ACACATCAAGAGTCCCGAGAGCGGTACTGACCCGCTGTCTCCGCGGAGAGCTGC 360
477 GCGTCTGAGGCTCAAGTTAAAGTGAGCAGCAGCTGAGCTATACAGAAATACAGCA 536
361 GTCGTGAGGCTCAAGTTAAAGTGAGCAGCAGCTGAGCTATACAGAAATACAGCA 420
537 ATGATTCCTGGCGCTACTACAGCAACCGGCTGCTGGCCCGAGTACCTACCGAGTGGC 596
421 ACAATTCCTGGCGATACCTACAGCAACCGGCTGCTGGCCCGAGCTGCGCAGAGTGGT 480
597 TGTCTTTGATGACCGGAGTGTGCGGAGTGTGAGCTGACCGCAGAGAGGCTATAGAG 656
481 TATCTTTGATGACCGGAGTGTGCGGAGTGTGAGCTGACCGCAGAGAGGCTATAGAG 540
657 GTTTCGCGCTAG-TGCCACTCTCTCTGACAGCAAAAGATACACACTCCAGCTGGAA 715
541 GCTTTCGCGCTTAGAGCGCCACTAGTCTGTGACAGAGGAT-ACACACTGCAAGTGAC 599
716 ATTAACGGGTTCAATTCGGCGCGCGGGGTGACCGCACCATTCAGCGCATGAACCG 775
600 ATCAACGGG-TCACTACCGGAGCGAGTGTGAGTGTGACCACTATGAGCATGAACCG 658
776 CCGTTCCTGCTCTACATGAGCCACCGCG--TGAGAGGGCCCGACCTGTCAAGCTCC 832
659 CTTTACTGCTTCTCAATGAGCACCGCGCATGAGAGGAGCCGATCTTGCAGAGCTCC 718
833 CGGACCGCGCGCGCTGATACCAACAGCTAC 865